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April 11, 2006, 02:03:38; Search time 112.845 Seconds (without alignments) 1608.075 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                - protein search, using sw model
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Title: Perfect score: Sequence:	US-09-037-657-13 2251 1 MPAGREGPVAQSARRPPRPLWRAWMQKSHKTRNQVLPAKL 413
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:

2443163

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aaw55011 Novel hae	Aay93658 A murine		Aaw55012 Novel hae	Aay93659 A murine		Aaw59804 Nucleotid	Aay26337 Murine U4		Aay29780 Mouse DNA		Mouse	Adc07180 Mouse cyt	Adt90845 Mouse cyt	Mouse	Mouse		Aay15214 Amino aci	Aay44839 Mouse orp	Human	Aab19588 Human cyt	Aab36647 Human cyt	Adc07179 Human cyt	Adt90844 Human cyt
SUMMARIES		ខា	AAW55011	AAY93658	AAE00820	AAW55012	AAY93659	AAE00821	AAW59804	AAY26337	AAW70862	AAY29780	AAB19589	AAB36648	ADC07180	ADT90845	ADT61033	ADY57158	ADZ65015	AAY15214	AAY44839	AAY29779	AAB19588	AAB36647	ADC07179	ADT90844
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ALIGNMENTS

Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; Mouse. Novel haemopoietin receptor NR6.1 protein. AAW55011 standard; protein; 413 AA (first entry) 29-SEP-1998 AAW55011; AMSSOILT 1
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(AMRA-) AMRAD OPERATIONS PTY LTD. (DZIE/) DZIEGLEWSKA H E. 97WO-GB002479. 96AU-00002246. WO9811225-A2. 11-SEP-1997; 11-SEP-1996; 19-MAR-1998.

Мив вр.

, Nicola NA, Farley A, Willson T, Zhang J, Alexander W; Fabri L, Kojima T, Maeda M, Kikuchi Y, Nash A; Hilton DJ, Nicola NA, WPI; 1998-260970/23. N-PSDB; AAV27140. Rakar S,

Claim 14; Page 77-81; 182pp; English.

neuronal cells.

New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g.

The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of the inference cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis,

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(revised)
                                                                                                                          Sequence 413 AA;
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                                                                                                                   ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH 120
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                                                                      1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
                                                                                 1 MPAGRPGPVAQSARRPPRPLSSLWSPLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
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predisposition to cancers, or
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The present sequence represents a murine haemopoietin receptor NR6 (CLF-polypeptide. The specification describes a method for the treatment or prophylaxis of disease conditions associated with dysfunctional haemopoietic regulation. The method comprises modulating the production of hemopoietic progenitor cells in a mammal by administration of NR6. Decreasing production of progenitor cells may be used in the treatment of cancer or to induce apoptosis of particular cell types. Increasing production of progenitor cells is used to facilitate postnatal survival in mammals by inducing or promoting suckling. Potential disease conditions may be identified by monitoring NR6 production in postnatal babies or allowing expectant mothers to undergo foetal testing. Low NR6 levels can then be treated immediately
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                                                                          (AMRA-) AMRAD OPERATIONS PTY LTD
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                     06-OCT-2000; 2000WO-AU001216
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Matches 413; Conservative
                                                                                                          Hasegawa M;
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                                                                                              Nash A,
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AAW55012 standard; protein; 425 AA

AAW55012

AAW55012
ID AAW5
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AC AAW5

RESULT 4

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Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                  Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicola NA, Parley A, Willson T, Zhang J, Alexander W, abri L, Kojima T, Maeda M, Kikuchi Y, Nash A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
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haemopoietin receptor NR6.2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Page 84-87; 182pp; English.
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                                                                                                                                                                                                                                                                                                                                          97WO-GB002479
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                                                                                                                                                                                                                                                                                                                                     11-SEP-1997;
                                                                                                                                                                                                                          WO9811225-A2
                                                                                                                                                                                                                                                                               19-MAR-1998.
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                                                                                                                                                                  Mus sp.
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The present invention relates to a biologically active complex comprising a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC). The complex is useful in the manufacture of a medicament for the treatment and/or prophylaxis of a subject, as it is involved in facilitating proliferation, differentiation and/or survival of a cell. The complex or its components have neurotrophic activity. The present sequence is murine haemopoietin receptor, NR6.2 isoform. The NR6.2 represents the NR6 splice variant obtained due to alternative mRNA splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New biologically active complex comprising NR6 and cardiotrophin-like-cytokine, for facilitating proliferation, differentiation and/or survival
                                                                                                                                    LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
                                                                                                                                                                                                                                                                                                                                                                                                        Murine; biologically active complex; haemopoietin receptor; NR6; cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation; differentiation; cell survival; neurotrophic activity.
         241 PPDVHVSRVGGLEDQLSVRWVSPFALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                          LAGLKPGTVYFVQVRCNPFGLYGSKKAGIWSEWSHPTAASTPRSERPGPGGVCEPRGGE
                                                   PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                    PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bartlett PF,
                                                                                                                                                                                                                                                                                                                                                                            Murine haemopoietin receptor, NR6.2 isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reid K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 26; Page 81-83; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330. .334
/label = WSXWS_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                         AAE00821 standard; protein; 425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMRA-) AMRAD OPERATIONS PTY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-2000; 2000AU-00007489.
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N-PSDB; AAD04193.
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Unidentified.
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Nakata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a cell.
                                                                                                                                                                                                                                                                                                        AAE00821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a murine haemopoietin receptor NR6 (CLF-1) polypeptide. The specification describes a method for the treatment or prophylaxis of disease conditions associated with dysfunctional haemopoietic regulation. The method comprises modulating the production of hemopoietic progenitor cells in a mammal by administration of NR6. Decreasing production of progenitor cells may be used in the treatment of cancer or to induce apoptosis of particular cell types. Increasing production of progenitor cells is used to facilitate postnatal survival in mammals by inducing or promoting suckling. Potential disease conditions may be identified by monitoring NR6 production in postnatal babies or allowing expectant mothers to undergo foetal testing. Low NR6 levels can then be treated immediately
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANINGSRQQSGDNLVCH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Administering the hemopoietin receptor NR6 is used to modulate production of hemopoietic progenitor cells and facilitate postnatal survival of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180
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                                                                                                                                                                                                                 Haemopoietin receptor NR6; CLF-1; dysfunctional haemopoietic regulation; hemopoietic progenitor cell; cancer; apoptosis; postnatal survival; suckling; postnatal baby; foetal testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
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               PSSGPVRRELKOFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ----VLPA 411
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Pred. No. 3.5e-184;
2; Mismatches 0; I
                                                                                                                                                                                         murine hemopoietin receptor NR6.2 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                             INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammals by inducing or promoting suckling.
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                                                                                                    Ą.
                                                                                                    AAY93659 standard; protein; 425
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98.8%;
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Best Local Similarity
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N-PSDB; AAA46792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 425 AA;
                                                                                                                                                                                                                                                                                                           WO200035471-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alexander WS,
                                                                                                                                                                                                                                                                                                                                                                                                                             (HALL-) HALL
                                                                                                                                                                                                                                                                                Mus musculus.
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haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant Up protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, cancer, and allergy)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine U4 protein; haematopoietin receptor superfamily; biological activity; cytokine; cell proliferation; cell differentiation; immune suppression; haematopoiesis regulation; immune disorder; immune deficiency; autoimmune disorder; allergy; cancer; myeloid cell; lymphoid cell deficiency; platelet disorder.
                                                                                                                                                                                                                                                                                                                                                                             61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANINGSRQOSGDNLVCH
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                                                                                                                                                                                                                   Length 425;
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                                                                                                                                                                                                                Score 2222.5; DB 2;
Pred. No. 7.8e-184;
2; Mismatches 1;
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/label= Putative_signal_sequence
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/label= Mature_murine_U4
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                                                                                                                                                                                                              Query Match 98.7%;
Best Local Similarity 98.6%;
Matches 408; Conservative
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                                                                                                                                                                               Sequence 425 AA;
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding U4 haematopoietin receptor superfamily charpotentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
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                                                                       ë,
                                    DB 4; Length 425;
                                                                       Indels
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                                  Score 2226.5; DB 4
Pred. No. 3.5e-184;
2; Mismatches 0;
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                                98.9%;
98.8%;
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                       Query Match
Best Local Similarity 98.8
Matches 409; Conservative
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425
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Sequence
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The present sequence represents a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to downregulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of zcytor5 could be used to detect cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                               mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-
llating Zcytor5 natural ligands or detecting cardiotrophin-1 in blood.
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cardiac pathology; heart enlargement; Zcytor5 ligand
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Pred. No. 1.1e-181;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                       Gilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulating Zcytor5 natural ligands or
                                                                                                                                                                                                                                                                                                                       Jelmberg AC,
Lehner JM;
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Best Local Similarity 97.6%;
Matches 404; Conservative
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Foster DC, Adams RL,
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13-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                   Novel polypeptides and polynucleotides used for treatment of human diseases and disorders e.g. immune disorders or deficiencies caused by fungal, parasitic or viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MPAGRAGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTFLIGSSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGFGGGVCEPRGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGODNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ----VLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2222.5; DB 2; Length 425; Pred. No. 7.8e-184; 2; Mismatches 1; Indels 3;
                                                                                                                    Neben T;
                                                                                                                    Σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
                                                                                                                     Whitters
                                                                                                                                                                                                                                                                                          Claim 9; Page 31-32; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW70862 standard; protein; 425
     99WO-US007882
                                            98US-00058660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 98.7%;
Best Local Similarity 98.6%;
Matches 408; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                 (GEMY ) GENETICS INST INC
                                                                                                                     Σ
                                                                                                                     Colling
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                                                                                                                                                          WPI; 1999-611303/52.
                                                                                                                                                                              N-PSDB; AAX90752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 425 AA
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                                            10-APR-1998;
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Length 425;

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309 PFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGCVCEPRGGEPSSGPVRRELKQFLGWL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine-like factor-1; CLF-1; interleukin-B60; IL-B60; mouse; cytokine; receptor; neuron; inflammation; antiinflammatory; autoimmune disease;
CHIPKDLALFIPYEIWVEATINELGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS
                                                                                                                                               VRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN
                                                                                                                                                                       249 VRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN
                                                                                                                                                                                                                                  PFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWL
                                                                 CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS
                                                                                                                                                                                                                                                                                                                                        369 KKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 405
                                                                                                                                                                                                                                                                                                                    KKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kastelein RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 21-22; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB19589 standard; protein; 407 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse cytokine-like factor-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-2000; 2000WO-US006182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00267901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Timans JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-587426/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 407 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2000,
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                          129
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                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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                       8 B
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                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a composition (I) comprising DNAX cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor subunit I (DCRS1) protein and DNAX soluble receptor subunit I (DCRS1) protein, which together encode a new mammalian cytokine related receptor (R), or DCRS1 and interleukin B30 (IL-B30) proteins, or DSRS1 and IL-B30 proteins, or DSRS1 and IL-B30 proteins, or DSRS1 and interleukin B30 (IL-B30) proteins, or DSRS1 and IL-B30 proteins, or compounds, which are useful for modulating the physiology or development of a cell or tissue culture e.g. inflammatory responses, innate immunity and/or morphogenic development. (R), antibodies and ligands are useful of for treatment of conditions exhibiting abnormal expression of (R): (R) is useful as a phosphate labeling enzyme to label substrates, and the subunits DSRS1 and DCRS1 are useful as immunogens for generating cutibodies, or as antigens for binding antibodies. Nucleic acids encoding (R) are useful for identifying related DNAs and mRNAs, and variants from other individuals or species. The present sequence represents the present individuals or species. The present sequence represents the present individuals or species. The present sequence represents the present individuals or species. The present sequence represents the present individuals or species are in the composition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 YWTLINGRRLPSELSRLLINTSTLALALANINGSRQQSGDNLVCHARDGSILAGSCLYVGLP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 YWTLNGRRLPSELSRLLNTSTLALALANLNGSRQOSGDNLVCHARDGSILAGSCLYVGLP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 PEKPFNISCWSRNMKDL:TCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 RPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 RPLSSLWSPLLLCVLGVPRGGSGAHTAVISPODPTLLIGSSLQATCSIHGDTPGATAEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New receptor subunits useful in the treatment inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                         interleukin B30; DSRS1; DCRS1; IL-B30; cytokine receptor; diagnosis; inflammatory disorder; inflammatory response; innate immunity; morphogenic development; immunological disorder.
                                                                                                                                                                                                                                                   soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.8%; Score 2134.5; DB 2; Length 416; 98.7%; Pred. No. 3.3e-176; ive 2; Mismatches 0; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kastelein RA;
                                                                                                                                                                                                          Mouse DNAX soluble receptor subunit 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 24-25; 133pp; English.
                                                                                AAY29780 standard; protein; 416 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0073941P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mcclanahan TK,
                                                                                                                                                                   (first entry)
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hes 392; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-527306/44.
N-PSDB; AAZ08862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention
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                                                                                                                                                                                                                                                                                                                                                                                                   WO9940195-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-FEB-1998;
13-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-PEB-1999;
                                                                                                                                                                   04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                            12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mattson JD,
                                                                                                                         AAY29780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                           Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                     DNAX
                                           RESULT 10
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The present sequence is that of mouse cytokine-like factor-1 (CLF-1), a cytokine receptor family protein, which forms a complex with human interleukin-B60 (IL-B60, see AAB19586). The IL-B60/CLF-1 cytokine serves as a key physiological factor in motor neuron development and regeneration. A claimed soluble complex comprises at least 6 amino acids of mature IL-60B, at least 6 amino acids of mature CNF-R. A claimed method of modulating the amino acids of mature CNF-R. A claimed method of modulating the contacting the cell with an agonist or antagonist of a complex comprising IL-60B and CLF-1 or CNFF-R. A claimed method of screening for a receptor which binds the complex involves contacting the complex into resoluting in a physiological response in the cell
Cytokine-like factor 1 (CLP-1) and interleukin (IL)-B60 complexes, polypeptides, and nucleic acids, useful in research, diagnosis and for treating inflammatory and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.1%; Score 2119; DB 3; Length 407;
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Bazan JF;

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317 299

179 257

119 197

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Local Best Loc Matches

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318 PRGIYGSKKAGIWSEWSHPTAASTPRSERPGGGGVCEPRGGEPSSGPVRRELKQFLGWL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    presence of their ligands and in drug screening assays. It is also useful for treating conditions such as immunological disorders. The present sequence represents a cytokine receptor subunit protein which is given in an alignment of various cytokine receptor subunits in the exemplification
                                                                                                                                                                                                                                                        YWTLNGRRLPSELSRLLNTSTLALALANINGSRQQSGDNLVCHARDGSILAGSCLYVGLP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 VRWYSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN
                                                                                                                                                                                                                                                                                                                       PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS
                                                                                                                                                                                                                                                                                                                                       120 PEKPFNISCWSRNMKDLTCRWTPGAHGETPLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS
                                                                                                                                                                                                                                                                                                                                                                                                     61 YWTLNGRRLPS-LSRLINTSTLALALANINGSRQQSGDNLVCHARDGSILAGSCLYVGLP
                                                                                                                                                                                                                                                                                                                                                                                    CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS
                                                                                                                                                                                                                            1 RPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGL
                                                                                                                                                                                           RPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGL
                                                                                                                                                              Gaps
                                                                                                                                                             4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunit 2; DCRS2; cell physiology;
culture; interferon detection;
                                                                                                                                                           0; Indels
                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kastelein RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ----VLPA 411
                                                                                                                                 4;
                                                                                                                             Score 2119; DB 4;
Pred. No. 7e-175;
2; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse cytokine receptor subunit NR7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gorman DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNAX cytokine receptor subunit 2; C cell development; cell culture; int immune system disorder; NR6; mouse.
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31-MAY-2000; 2000US-00588113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-2002; 2002US-00247463
                                                                                                                                 94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC07180 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                Best Local Similarity 98.5
Matches 391; Conservative
                                                      an alignment or various of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIMANS J C.
GORMAN D M.
KASTELEIN R A
BAZAN J F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOWLING L M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003082734-A1.
                                                                                                   Sequence 407 AA;
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(TIMA/)
(GORM/)
(KAST/)
(BAZA/)
                                                                                                                                    Query Match
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ADC07180
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                                                                                                                                    120 PEKPFNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS
                                                                            RPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGL
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                                                                                                                                                                                                                                                CHIPKDLALFTPYEIWVEATWRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNAX cytokine receptor subunit; DCRS2; receptor protein; modulating cell proliferation; diagnosis; detection; drug immunological disorder.
                        Indels
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Mismatches
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                                                                                                                                                                                                                                         The invention describes a composition of matter (I) comprising a substantially pure or recombinant DMAX cyrckine receptor subunit 2 (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion protein comprising a DCRS2 sequence. A composition of matter comprises: a comprising a DCRS2 sequence. A composition of matter comprises: a ubstantially pure or recombinant DCRS2 polypeptide comprising at least to thur amino acids identical to segments of at least four amino acids identical to segments of a substantially pure or recombinant DCRS2 comprising at least two distinct nonverlapping segments of at least two distinct nonverlapping segments of at least two distinct nonverlapping segments of at least two distinct nonverlapping segmence. CC hardonist of a mategoist of a mammalian DCRS2 is useful for modulating physiology or development of a cell or cell culture. Antibodies to a DCRS2 can be used for quantitative detection of interferon. The DCRS2 polypeptides and nucleic acids and their binding agents are potentially useful in treating and diagnosing disease, especially disease associated with the immune system. This is the amino acid sequence of mouse cytokine receptor subunit NRG used in a comparision with DCRS2.
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                                                                     Composition potentially useful for treating immunological disorders, comprises a DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion polypeptide comprising a DCRS2
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                                                                                                                                                                                               Disclosure; SEQ ID NO 5; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a complex comprising interleukin (IL)-B60, cytokine-like factor 1 (CLF-1) (partner sequence of IL-B60) and CNTF-R (CNTF-receptor). The complex is useful for producing an antigen:antibody complex, useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions and/or autoimmune disorders and for generating antibodies which is useful in diagnostic applications. The present sequence is mouse cytokine-like factor 1 (CLF-1).
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;
Interleukin; IL-B60; cytokine-like factor 1; CLF-1; CNTF-R;
CNTF-receptor; inflammatory condition; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 407;
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Pred. No. 7e-175;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bazan JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kastelein RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 13; 41pp; English.
                                                                                                                                                                                                                                                                                          11-FEB-2004; 2004US-00778002
                                                                                                                                                                                                                                                                                                                                                       11-MAR-1999; 99US-0124319P, 09-MAR-2000; 2000US-00521335,
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98.5%;
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Matches 391; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to mammalian interleukin-B60 (IL-B60). The invention also provides a method of producing a soluble complex comprising the mature protein portrions of IL-B60 and CLP-1 polypeptides. The methods and compositions of the present invention are useful in controlling biology and physiology of mammalian invention are useful in controlling biology and physiology of mammalian cells, such as cells of mammalian immune system, and in particular for regulating activation, development, differentiation and function of various cell types, including haematopoietic cells. They are specifically useful in treating abnormal medical conditions, including immune disorders, such as T cell immune deficiency, chronic inflammation or tissue rejection, or in cardiovascular or neurophysiological conditions. The present sequence is the mouse cytokine-like factor 1 (CLP-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated or non-human host cells transfected with expression vectors having nucleic acids encoding cytokines, useful in treating immune disorders, cardiovascular or neurophysiological conditions.
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                                                                                                                                                Cytokine; interleukin-B60; IL-B60; cell physiology; immune system; haematopoietic cell; immune disorder; T cell immune deficiency; chronic inflammation; tissue rejection; cardiovascular condition; neurophysiological condition; mouse; cytokine-like factor 1; CLF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.1%; Score 2119; DB 8; Length 407; 98.5%; Pred. No. 7e-175; ive 2; Mismatches 0; Indels
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                                                                                                                 Mouse cytokine-like factor 1 (CLF-1).
                ADT61033 standard; protein; 407 AA.
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                                                                                 (first entry)
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Matches 391; Conservative
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Search completed: April 11, 2006, 02:09:56 Job time : 113.845 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

April 11, 2006, 02:10:19 ; Search time 20.6664 Seconds (without alignments) 1922.808 Million cell updates/sec Run on:

US-09-037-657-13 2251 1 MPAGRPGPVAQSARRPPRPL......WRAWMQKSHKTRNQVLPAKL 413 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% 'Listing first 45 summaries

Database

PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	prolactin receptor	prolactin receptor	prolactin receptor	membrane glycoprot	glycoprotein 130 -	interleukin-6 sign	rec	prolactin receptor	prolactin receptor	lactogen receptor	prolactin receptor		prolactin receptor		prolactin receptor		prolactin receptor	prolactin receptor		granulocyte colony	granulocyte colony	granulocyte colony	ciliary neurotroph	ciliary neurotroph	interleukin-11 rec	interleukin-11 rec	growth promoting a	interleukin-6 rece	interleukin-6 rece
	:	ai	B59405	A59405	A40144	A36337	149699	A44257	I50455	A29884	A41070	A34631	A36116	177525	177524	153269	A30304	JQ1655	145971	151086	B38252	JH0329	C38252	A34898	I58141	UHHUCN	137891	I48343	S60614	JL0145	A41242
	á	BB	7	7	7	~	N	~	~	~	~	7	~	~	~	7	~	~	~	~	~	7	~	~	~	Н	~	~	~	~	-
		Length	288	376	622	918	917	918	830	310	412	610	610	292	303	608	616	831	581	630	771	783	863	837	372	372	422	432	362	460	468
de	Query	Match	14.7	14.7	14.7		14.2	14.1		13.9	13.9	13.9	.13.9	13.7	13.7	13.7	13.7	13.6	13.4	11.6	11.3	11.3	11.3	11.2	10.4	9.8	9.3	9.3	9.5	0.6	8.9
		Score	331	331	331	329	319.5	317.5	314	312	312	312	312	307.5	307.5	307.5	307.5	306	302.5	261.5	254.5	254.5	254.5	252.5	234	220.5	209.5	208.5	0	203.5	200.5
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126 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184

15 LPLNTCLINGQLPPGKDEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72

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244 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 298

299 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342

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prolactin receptor interleukin-6 rece	MPL-K protein prec MPL-P protein prec leptin receptor, s	leptin receptor, s leptin receptor, s leptin receptor, s	leptin receptor, s lactogen receptor hematopoletic grow	leukemia inhibitor leptin receptor, O	<pre>proto-oncogene - m differentiation-st leptin receptor, i</pre>
A32868 JL0144	845266 84841	S68439 S68437 S68440	S68438 B34631 S35317	S17308 PC4184	S37622 JX0312 S74225
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156 440	635 805 805	892 894 900	1162 150 625	1097	626 1092 895
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199	192.5	191.5 191.5 191.5	191.5 190 190	190 188.5	186 185 182
30	1 E E	35 36 37	8 6 7 8 6 0	417	4 4 4 5 4 4

ALIGNMENTS

RESULT 1 B59405 problactin receptor short form S1b precursor, breast cancer cells T-47D - human C190-lactin receptor short form S1b precursor, breast cancer cells T-47D - human C19Decies: Homo sapiens (man) C19Decies: Homo sapiens (man) C19Decies: 01-Feb-2002 #sequence revision 01-Feb-2002 #text_change 09-Jul-2004 C19Ccession: B59405; B49400 T19M.L. 3.75. Meng, J.; Duffau, M.L. J. Biol. Chem. 276, 41086-41094, 2001
A;Title: Isolation and characterization of two novel forms of the human prolactin recep A;Reference number: A59405; MUID:21538812; PMID:11518703 A;Accession: B59405 A;Status: preliminary A;Anolecule type: DNA b; Disciplinary A;Anolecule type: DNA b; Disciplinary A;Anolecule type: DNA b;Anolecule type: DNA b;Disciplinary A;Anolecule type: DNA b;
A;Cross-references: 1-200 chor. A;Cross-references: UNIPROT:Q96P36; UNIPARC:UPI00006CDDA; GB:AF214012; PIDN:AF214012.1 R;Hu, Z.Z. submitted to GenBank, December, 1999 A;Reference number: A49400 A;Accession: B49400
A;Status: preliminary A;Molecule type: DNA A;Rosidues: 1-288 et al. A;Rosidues: 1-288 et al. A;Coss-references: UNIPARC:UPI00006CDDA; GB:AF214012; PIDN:AF214012.1 C;Comment: This is one of the short forms (Sla and Slb) of the human proactin receptor tar-assein gene promoter activation, with Slb more effective than Sla. However, their li C;Genetics:
A;Gene: GDB:PRLR A;Cross-references: GDB:120315; OMIM:176761 A;Map position: 5p13.3-5p13.1 C;Keywords: glycoprotein; transmembrane protein C;Keywords: glycoprotein; transmembrane predicted <sig> F;1-24/Domain: signal sequence #status predicted <sig> F;2-288/Product: prolactin receptor, short form S1b #status predicted <mat> F;36-221/Domain: cytokine receptor homology <grs> F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted</grs></mat></sig></sig>
Query Match Best Local Similarity 37.5%; Pred. No. 2.7e-18; Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

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A; Residues: 1-622 <BOU>
A; Cross-references: UNIPROT:P16471; UNIPARC:UPI0000132234; GB:M31661; NID:g190361; PIDN: B; Pub, G.; Wells, J.A.
J. Biol. Chem. 270, 1313-13137, 1995
A; Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li
A; Reference number: A57018; MUID:95286597; PMID:7768908
A; Accession: A57018; MUID:95286597; PMID:7768908
A; Reference number: A57018; MUID:95286597; PMID:7768908
A; Residue: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: MRNA
A; Residues: 25-228, AW' <RES>
A; Cross-references: UNIPARC:UPI000006D208; GB:S78505; NID:g999114; PIDN:AAB334470.1; PID: C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane glycoprotein gpl30 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
C;Accession: A36337
R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an IL-6 signal transducer, gpl30.
A;Reference number: A36337
A;Accession: A36337
A;Retus: preliminary
A;Residues: 1-918 <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 LANLINGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 ISPESPVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVT 90
                                                                                                                                                                                                                                                                                                                                                    A)Gene: GDB:PRLR
A)Gene: GDB:120315; OMIM:176761
A)Gene: GDB:120315; OMIM:176761
A)Gene: CDB:120315; OMIM:176761
A)Gene: GDB:120313.1
C)GENE-CONTENT SPIN:1
C)GENE-CONTENT SPIN:1
C)GENE-CONTENT SEGUENCE #Status predicted <SIG>
C)GENE-CONTENT POLACTIN receptor, long form #status predicted <MAT>
C)36-221/Domain: cytokine receptor homology <CRS>
C)55-21/Domain: cytokine receptor homology <CRS>
C)59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 37.5%; Pred. No. 7.1e-18;
Matches 84; Conservative 27; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Match
Local Similarity 28.6%; Pred. No. 1.6e-17;
tes 88; Conservative 51; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
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C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:126725; OMIM:600694
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Best Local S:
Matches 88
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A,Accession: A49400
A,Status: preliminary
A,Status: preliminary
A,Residues: 1-376 <HU2>
A,Cross-references: UNIPARC:UPI000006E673; GB:AF214012; PIDN:AF214012.1
C,Comment: This is one of the short forms (Sla and Slb) of the human prolactin receptor eta-casein gene promoter activation, with Sia less effective than Slb. However, their lited COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe
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C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Datession: A40144; A57018
R;Boutin, J.M.; Edery, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D. Mol. Endocrinol. 3, 1455-1461, 1989
A;Title: Identification of a cDNA encoding a long form of prolactin receptor in human layreternece number: A40144; MUID: 90114212; PMID: 2558309
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Map position: 5p13.3-5p13.1
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein; transmembrane proticed <SIG>
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-376/Product: prolactin receptor, short form S1a #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                              prolactin receptor short form Sla precursor, breast cancer cells T-47D - hur C;Species: Homo sapiens (man)
C;Species: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 NICEEYHIVGPHSCHIPKD-LALFIPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS
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                    ---DHGYWSAWSPATFIQIP 227
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A;Gene: GDB:PRLR
A;Cross-references: GDB:120315; OMIM:176761
              191 FKILSLHPGQKYLVQVRCKP---
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Matches 84; Conserv
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R;Chen, X.; Horseman, N.D.
Bidocrinology 135, 269-276, 1994
A;Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor. A;Reference number: 150455; MUID:94283267; PMID:7516866
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                                                                                                                                C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R;Wang, Y:, Neabitt, J.B.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A;Title: Molecular cloning and characterization of the rat liver IL-6 signal tra
A;Reference number: A44257; MUID:93052397; PMID:1427893
A;Accession: A44257
A;Status: preliminary: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-918 «WAN>
A;Residues: 1-918 «WAN>
A;Residues: 1-918 «WAN>
A;Residues: Univer
A;Note: sequence extracted from NCBI backbone (NCBIP:118488)
C;Keywords: transmembrane protein
F;134-315/Domain: cytokine receptor homology <CRS>
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C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 HGETFLHTNYSLKYKLRWYGOD-NTCEEYHTVGPHSCHIPKDLALFTPYBIWVBATWRLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.1%; Score 317.5; DB 2;
29.8%; Pred. No. 1.3e-16;
tive 51; Mismatches 145;
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                                                                                                             interleukin-6 signal transducing molecule gp130
C;Species: Rattus norvegicus (Norway rat)
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Best Local Similarity 37.18
Local Similarity 37.18
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Matches 92; Conserva
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A; Residues: 1-830 < CHE>
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                                                                                                                                                                                                                                                                                      207 VISDHINPDPVYKVKPNPPHILSVINSBELSSILKLIWTN-PSIKSVII-LKYNIQYRTK 264
                                                                                                                                                                                                                                                                                                                                                                                        DSVDWKVV---DDVSNQTSCRLAGIKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                 265 DASTWSQIPPEDTASTRSSFTVQDLKPPTEYVFRIRC----MKEDGKGYWSDWSEEASG 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ETYLBINYTLKSE--WATEKFPDCQSKHGT---SCMVSYMPTYYVNIEVWVEAENALG 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SARSDVLTLDVLDVVTTDPPPDVHVSRVGGLBDQLSVRWVSPPALKDFLFQAKYQIRYRV 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90
                                                                                                          HGETFLHTNYSLKYKLRWYGODNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATURLGS
                                                                                                                                                         -- BTHLETNFTLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 IYPEPPVVQRGSNFTAICVLKEACLQHYYVNASYIVWKTNHAAVPREQVTVINRTISSVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AST--PRSERP 347
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A,Accession: I55417
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A;Rebidues: 1-412 cRES>
A;Cross-references: UNIPARC:UP1000002B19B; EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PICAS,Experimental source: ND2-11C cell line
C;Keywords: transmembrane protein
F;31-216/Domain: cytokine receptor homology <CRS>
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A34631
R;Zhang, R.; Buczko, B.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Biochen: Biophys. Res. Commun. 168, 415-422, 1990
A;Fitle: Isolation and characterization of two novel rat ovarian lactogen receptor c A;Fitle: Isolation and characterization of two novel rat ovarian lactogen receptor c A;Ference number: A34631; MUID:90241201; PMID:2159291
A;Accession: A34631
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A;Residues: 1-610 < ZIM>A;Residues: 1-610 < ZIM>A;Resi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 NT--CEEYHTVGPHSCHIPKD-LALFIPYEIWVEATNRLGSARSDVITLDVLDVVTTDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 TOPKVFDLYPGQKYLVQTRCKP-----DHGYWSRWSQESSVEMP 222
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                                                                                                                                                                                                                                                                                                                                             Length 412;
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A; Reference number: 155417; MUID: 95014432; PMID: 7929319
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                                                                                                                                                                                                                                                                                                                                             , DB 2;
1.3e-16;
                                                                                                                                                                                                                                                                                                                        13.9%; Score . 35.4%; Pred. No. 1.3e-1.1ve 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prolactin receptor 2 precursor
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prolactin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A29884
C;Accession: A29884
R;Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banville
Call 53, 69-77, 1988
A;Title: Cloning and expression of the rat prolactin receptor, a member of the growth hc
A;Reference number: A29884; MUD:88165059; PMID:2832068
A;Rolecule type: mRNA
A;Residues: 1-310 <BOUS
A;Residues: 1-310 <BOUS
A;Residues: Lransmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-310/Product: prolactin receptor #status predicted <NAT>F;31-216/Domain: cytokine receptor homology <CRS>
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Cispecies: Rattus norvegicus (Norway rat)
Cjoace: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 09-Jul-2004
Cjoace: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 09-Jul-2004
Cjoace: 15-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 09-Jul-2004
Cjoace: 15-Jul-1992 #sequence_revision 12-Jun-1992 #text_change 09-Jul-2004
Rial; S.; Pellegrini, I.; Kelly, P.A.
Rial; S.; Pellegrini, I.; Kelly, P.A.
A; Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolact
A; Reference number: A41070; MUID:92041834; PMID:1718958
A; Reference number: A41070
A; Residues: 1-412 < ALL:
A; Residues: 1-412 < ALL:
A; Residues: L.Y.
A; Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19B; GB:M74152; NID:g206389; PIDN:
A; Cross-references: L.Y.
A; Ritle: Differential signal transduction of the short, Nb2, and long prolactin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 NSCYFDKKHTSFWIIYNITVKATNEIGSNVSDPLYVDVTYIVQTDPPVNVTLELKKTVNR 347
                                                                                                                                                                                                                                                                                 348 KPYLVITW-SPPPLADVRSGWLTLDYELRLKPEEAEEWETI-FVGQQTHYKMFSLNPGKK 405
   PPEKPILIKCRSPEKETFTCWWKPGSDGG---HPTNYTLLYSKEGEERVYECPDYKTAGF 287
                                                                                                          HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDV--HVSRVGGL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK
                                                                                                                                                                                                                                                 EDQLSVRWVSPPALKDF - - - LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :: | | | | | | | | | | | TOPKVFDLYPGQKYLVQTRCKP-----DHGYWSRWSQESSVEMP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                    310 YFVQVRCNPFGIYGSKKAGIWSEWS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 YIVQIHCKP-----DHHGSWSEWS 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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A; Molecule type: mRNA
A; Residues: 1-608 <RES>
A; Residues: 1-608 <RES>
A; Cross-references: UNIPROT: Q08501; UNIPARC: UPI0000020E90; GB: L14811; NID: G293769; PIDN
R; Moore, R.C.; Oka, T.
Gene 134, 263-265, 1993
A; Title: Cloning and sequencing of the CDNA encoding the murine mammary gland long-form
A; Reference number: JT0671; MUID: 94085788; PMID: 8262385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q08501; UNIPARC:UP1000002B197; GB:M22958; NID:g200479; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prolactin receptor, long form - mouse Cispecies: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004 C; Accession: I33269; JT0671; S34356 R; Clarke, D.L.; Linzer, D.I.H. Bidocrinology 133, 224-212, 1993 A; Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary. A; Reference number: I53269; MUID:93307149; PMID:8319571
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A.Residues: 1-608 <MOO>
A.Cross references: UNIPARC:UPI000020E90; GB:L13593; NID:g347398; PIDN:AAC37641.1;
A.Cross references: Mandi, S.; Kelly, P.A.
Submitted to the EMBL Data Library, June 1993
A.Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 WKIYIITUNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLMVKMLPP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT--CBEYHTVGPHSCHIPKD-LAL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 FTPYEIWVEATURLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--PP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 ALKOF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PPGKPEIHKCRSP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 DKETFTCWWNPGSDGG--LPTNYSLIYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 TITDVKTGWFTMEXBIRLKSBEADEWE-IHFTGHQTQFKVFDLYPGQKYLVQTRCKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.7%; Score 307.5; DB 2; Length 303; 32.6%; Pred. No. 1.9e-16;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 YGSKKAGIWSEWSHPTAASTP 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85; Conservative
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A; Reference number: S34356
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                                                    Cincession: A3616
Rishirota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, J. A; Shirota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, J. A; Title: Expression of two forms of prolactin receptor in rat ovary and liver.
A; Reference number: A36116; MUD: 91155946; PMID: 2293022
A; Accession: A36116
A; Status: preliminary
A; Molecule type: mRNA
A; Residue: 1-610 cSH1>
A; Residue: 1-610 cSH1>
A; Residue: 1-610 cSH1>
A; Cross-references: UNIPROT: P05710; UNIPARC: UP10000170ADB; GB: M57668; NID: 9206366; PIDN: F;31-216/Domain: cytokine receptor homology cCRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Wis musculus (house mouse)
C;Species: Wis musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: 13,7525
Molecule: Expression of multiple forms of the prolactin receptor in mouse liver.
A;Reference number: 157699; MUID:89261824; PMID:2725531
A;Accession: 177525
A;Accession: 177525
A;Accession: 177525
A;Accession: 177525
A;Accession: 177525
A;Accession: NUMA
A;Residues: 1-292 cRES>
A;Cross-references: UNIPROT:Q08501; UNIPARC:UP1000002B198; GB:M22959; NID:g200481; PIDN:F;31-216/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 SILAGSCLYVGLPPEKPFNISCWSRNMKDLICRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 LSRLLINTSTLALALANINGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 TITDVKTGWFTMEYEIRLKSEEADEWE-IHFTGHQTQPKVFDLYPGQKXLVQTRCKP--- 205
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Species: Rattus norvegicus (Norway rat)
Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prolactin receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          13.9%; Score 312; DB 2;
Similarity 35.4%; Pred. No. 2.1e-16;
10; Conservative 35; Mismatches 85,
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Best Local Simi
Matches 80;
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A; MCCOULE type: MRNA
A; Residues: 1-57, F', 559-608 <EDE>
A; Residues: 1-57, F', 559-608 <EDE>
A; Cross-references: UNIPARC:UPIO000163B24; EMBL:X73372; NID:g312696; PIDN:CAA51789.1; PI
C; Comment: Prolactin receptor have long form and short form which are resulted from alte
C; Comment: This long form receptor is capable of transducing a signal to milk protein ge
C; Reywords: receptor; transmembrane protein
F; 31-216/Domain: cytokine receptor homology <CRS>
F; 230-253/Domain: transmembrane #status predicted <TWM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prolactin receptor 2 precursor - rabbit
N'Alternate names: prolactin receptor, mammary gland
C;Species: Orycolagus cuniculus (domestic rabbit)
C;Decies: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: A30304; A60380
C;Accession: A30304; A60380
R;Edery, M.; Jolicoeur, C.; Levi-Meyrueis, C.; Dusanter-Fourt, I.; Petridou, B.; Boutin, Proc. Natl. Acad. Sci. US.A. 86, 2112-2116; 1989
A;Title: Identification and sequence analysis of a second form of prolactin receptor by A;Reference number: A30304; MUID:89184578; PMID:2928321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: protein
A, Residues: 41-58, X, 60-66,90-93, X, 95-96, X, 98-103, X, 105, XX, 108,150-164, XX, 167
A, Residues: 41-58, X, 60-66,90-93, X, 95-96, X, 98-103, X, 105, XX, 108,150-164, XX, 167
A, Cross-references: UNIPARC:UPI000017C5D9; UNIPARC:UPI000017C5DB;
A, Note: the amino end of the mature protein was blocked
C, Keywords: blocked amino end; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;5-61/Product: prolactin receptor 10mology <CRS>
F;5-61/Product: prolactin receptor homology <CRS>
F;25-58/Domain: cytokine receptor homology <CRS>
F;25-28/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A30304
A;Molecule type: mRNA
A;Residues: 1-616 <EDE>
A;Cross-references: UNIPROT: P14787; UNIPARC: UPI0000132237; GB:J04510; NID:g165669; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
Int. J. Blochem. 22, 1089-1095, 1990
A;Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor
A;Reference number: A60380; MUID:91146782; PMID:2289615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;235-258/Domain: transmembrane #status predicted <TMM>
;59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 ALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 NMKDLICRWIPGAHGEIFLHINYSLKYKLRWYGQDNI--CEEYHTVGPHSCHIPKD-LAL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 FTPYEIWVEATURLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--PP 264
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                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                          Query Match
13.7%; Score 307.5; DB 2
Best Local Similarity 32.6%; Pred. No. 4.6e-16;
Matches 85; Conservative 37; Mismatches 92
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Best Local Similarity
Matches 77; Conserv
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SCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVTTDPPPPDVHVSRVGGLEDQ 255
                                                                                                               LSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVY 310
                                                                                                                                            85 SCYPSKKHTSIWTIYIITYNATNQMGSSVSDPRYVDVTYIVBPDPPVNLTL-EVKHPEDR
                                                                                                                                                                                                                               311 FVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                     203 LVQVRCKP-----DHGFWSVWSPESSIQIP
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Search completed: April 11, 2006, 02:17:26 Job time : 21.6664 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 11, 2006, 02:04:23 ; Search time 123.014 Seconds (without alignments) 2368.694 Million cell updates/sec Run on:

US-09-037-657-13 2251

Title: Perfect score:

1 MPAGRPGPVAQSARRPPRPL........WRAWMQKSHKTRNQVLPAKL 413 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q9jm58 mus musculu	075462 homo sapien		Q6uaq5 tetraodon n	Q4rmp5 tetraodon n	Q4tcm7 tetraodon n	Q4rdr1 tetraodon n	Q4rdq9 tetraodon n	Q9w6u9 gallus gall	057519 xenopus lae		Q96p36 homo sapien	homo	рошо	homo	pongo	Q7tq89 rattus norv	рошо	P40189 homo sapien	mus n	Q6pdi9 mus musculu		Q9n0j7 callithrix	Q99jz1 mus musculu			Q58dz7 rattus norv	P05710 rattus norv	Q8c7gl mus musculu	Q08501 mus musculu	P14787 oryctolagus
SUMMAKIES	ID	CRLF1 MOUSE	CRLF1 HUMAN	Q6DG28 BRARE	Q6UAQ5_TETNG	Q4RMP5 TETNG	Q4TCM7_TETNG	Q4RDR1_TETNG	Q4RDQ9_TETNG	Q9W6U9 CHICK	057519_XENLA	Q8TD78_HUMAN	Q96P36_HUMAN	Q9UHJS HUMAN	Q96P35 HUMAN	PRLR HUMAN		Q7TQ89_RAT	Q5FC04_HUMAN	ILGRB_HUMAN	IL6RB_MOUSE	Q6PDI9_MOUSE	IL6RB_RAT	Q9N0J7_CALJA	Q99JZ1_MOUSE	Q865V4_CEBAP	PRLR_COLLI	Q58DZ7_RAT	PRLR_RAT	Q8C7G1 MOUSE	PRLR MOUSE	PRLR_RABIT
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ا ع	Match	98.9	93.1	63.2	61.4	44.2	20.8	18.5	16.9	16.5	15.8	14.7	14.7	.14.7	14.7	14.7	14.7	14.7	14.6	14.6	14.2	14.2	14.1	14.0	14.0	13.9	13.9	13.9	13.9	13.7	13.7	13.7
	Score	2226.5	2096	1422.5	1382.5	995	468.5	416	380	~	355.5	332	331	331	331	331	331	330.5	329	329	319.5	319.5	317.5	316	314.5	Н	314	312	312	307.5	307.5	307.5
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ALIGNMENTS

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                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW
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                                                                                                                                                                          HSSP; P40223; 1CD9.
Ensembl; ENSWUSG0000007888; Mus musculus.
MGI: MGI:1340030: cxtracellular space; TAS.
GO: GO:0005615; c:xtracellular space; TAS.
InterPro; IPR00296; Cytkn recept_B/G.
InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
Pfam; PF00041; fn3; 2.
SWART; SM00066; FN3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50853; GIXE; FALSE NEG.
Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
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Phosphoserine.
N-linked (GlCNAc...) (F N-
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Fibronectin type-III 1.
Fibronectin type-III 2.
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2; Mismatches 0;
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                                                                                                                                                             EMBL; AB040038; BAA92777.1; -; mRNA.
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Best Local Similarity 98.8
Matches 409; Conservative
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187
125 AA;
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                      domain.
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MUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

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Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

Raton D., Roster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Kilmowski L., Jin Y., Johnson S., Lee J.,

Lewis D., Liao D., Mark M.R., Robbie B., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

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Mood W.L., Godowski P.J., Gray A.M.;

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The fefort to identify novel human secreted and transmembrane proteins: a

print pioinformatics assessment.";
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MEDLINE=22388257, PubMed=12477932, DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A plachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Parage C.,

Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

Rillalon D.K., Marusy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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Rakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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SPECIFICITY, AND INDUCTION.
TISSUE=Petal lung;
MEDILINE=98349389; PubMed=9686600;
Elson G.C.A., Graber P., Losberger C., Herren S., Gretener D.,
Menoud L.N., Wells T.N.C., Kosco-vilbols M.H., Gauchat J.-F.;
"Cytokine-like factor-1, a novel soluble protein, shares homology with
members of the cytokine type I receptor family.";
                                                                                                                                                                                                                                                                                                                                                                                                              nouso septens (namenn).
Bukaryota, Merazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1) (CLF-1) (2cytoR5).

Name=CRLF1; Synonyms=ZCYTOR5; ORFNames=UNQ288/PRO327;

Homo sapiens (Human).
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                                                                                                                                                     Last sequence update)
Last annotation update)
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CRLFI HUMAN STANDARD;
075462; Q9UHH5;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last seq
13-SEP-2005 (Rel. 48, Last ann
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                feral lung.

IMDUCTION: Up-regulated in fibroblast primary cell cultures under stimulation by IRV-gamma, TRY-alpha and IL-6.

DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.

BISBASE: Defects in CRLF1 are the cause of cold-induced sweating syndrome (CISS) [MIM:272430]. CISS is an autosomal recessive disorder characterized by profuse sweating induced by cool source characterized by profuse sweating induced by cool abnormalities include a high-arched palate, nasal voice, depressed nasal bridge, inability to fully extend the elbows and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Cytokine receptor subunit, possibly playing a regulatory role in the immune system and during fetal development. May be involved in nervous system development.

SUBUNIT: Forms covalently linked di- and tetramers. Forms a heteromeric complex with cardiotrophin-like cytokine (CLC); the CELFI/CLC complex is a ligand for the ciliary neurotrophic factor receptor (CNTFR).

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Highest levels of expression observed in spleen, thymus, lymph node, appendix, bone marrow, stomach, placenta, heart, thyroid and ovary. Strongly expressed also in
'Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22428294; PubMed=12509788;
Knappskog P.M., Majewski J., Livneh A., Nilsen P.T.E., Bringsli J.S.,
Ott J., Boman H.;
                                                                                                                                                                                                                                                                                                                                                            Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Itt J., Boman \mu.;
'Cold-induced sweating syndrome is caused by mutations in the CRLP1
                                                                                                                                                                                                                                                                                         INTERACTIONS WITH CLC AND CNTFR.

MEDLINE=20423191; PubMed=10966616; DOI=10.1038/78765;

Elson G.C.A., Lelievre E., Guillet C., Chevalier S., Plun-Favreau Froger J., Suard I., de Coignac A.B., Delneste Y., Bonnefoy J.Y., Gauchat J.-F., Gascan H.;

"CLF associates with CLC to form a functional heteromeric ligand f the CNTF receptor complex.";
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                                                                                                  PROTEIN SEQUENCE OF 38-52.

PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;

"Signal peride prediction based on analysis of experimentally verified cleavage sites.";

Protein Sci. 13:2819-2824(2004).
                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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VARIANTS CIȘS HIS-81 AND ARG-374
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AY358291; AAQ88658.1; -;
BC044634; AAH44634.1; -;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGODNTCEEYHTVGPHSCHI PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPDVHVSRVGGLEDQLSVRWVSPPALKDPLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411
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                                                                                                                                                           Pfam; PR00041; fn3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50835; IG_LIKE; FALSE NEG.
Direct protein sequencing; Disease mutation; Glycoprotein;
Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
(Potential).
(Potential).
(Potential).
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GO:0005615; C:extracellular space; TAS.
GO:0019955; F:cytokine binding; IPI.
GO:0004872; F:receptor activity; TAS.
GO:0019735; P:antimicrobial humoral response (sensu Verte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                            Cytokine receptor-like factor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphoserine (By similarity).
N-linked (GlcNac. .) (Potenti
By similarity.
By similarity.
F -> H (in CISS).
FTIG=VAR 017865.
L -> R (in CISS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTId=VAR 017866.
-> E (in Ref. 3).
AD9DEFCB01B84228 CRC64;
                                                                                                                                                                                                                                                                                                                             ig-like C2-type.
Fibronectin type-III 1.
Fibronectin type-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; DB 1;
4.3e-158;
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; Pred. No. 4.3e-:
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      WSXWS motif.
                                                                                            InterPro, IPR002996; Cytkn recept_B/G.
InterPro, IPR003961; FN III.
InterPro, IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created
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QEDG28;
25-OCT-2004 (TrEMBLrel. 26
25-OCT-2004 (TrEMBLrel. 26
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Q6DG28 BR
ID Q6DG
AC Q6DG
DT 25-C
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98
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Straubberg R. D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I-DOMAIN: The WEXWAS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).

EMBL: BC076526; AAH76526.1; -; mRNA.

ZFIN; ZDB-GENE-040718-397; zgc:91992.

InterPro; IPR002996; Cytkn recept_B/G.

InterPro; IPR002996; Cytkn recept_B/G.

Ffam; PR0014; fn3; 1.

SMART; SM00060; FN3; 2.

PROSITE; PSS0085; FN3; 2.

Receptor; Repeat; Transmembrane.

SEQUENCE 389 AA; 43314 MW; E30903B99639864A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 LLLCVLGVPRGGSGAHTAVISPODPTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 PSELSRLLMTSTLALALANIAGSRQQSGDNLVCHARDGSILAGSCLXVGLPPEKPFNISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 WSRNMKDLTCRWTPGAHGETFLHTNYSLKYKCLRWYGQDNTCEEYHTVGPHSCHIPKDLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTPYEIWVEATURLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                             7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.2%; Score 1422.5; DB 2; Length 389; 68.2%; Pred. No. 1.4e-104; ive 48; Mismatches 67; Indels 7;
                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (UUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA
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Nucled S., Jaffe D., Fisher C., Cout-Costaz C., Bernot A.,

Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

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R. Anthouard V., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

R. Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

R. Alindblad-Toh K., Birren B., Nusbaum C., Rahn D., Robinson-Rechavi M.,

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T. the early vertebrate proto-karyotype.";

Nature 431:946-957(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKOFLGWLKKHAY-CSN 385
                                   27 LLLCVI,GVPRG-GSGAHTAVISPODPTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- DOMAIN: The WSXMS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).

EMBL, AY374473; AR2564.1; -; mRNA.

ENBEMD1, AY374473; Tetraodon nigroviridis.

GO, GO:0004872; F:receptor activity; IEA.

InterPro; IPR001996; Cytkn_recept_B/G.

InterPro; IPR00110; III.

InterPro; IPR00110; III.

Ffam; PF00041; fn3; 2.

SMART; SM00060; FN3; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodon nigroviridis (Green puffer).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha; Acanthopterygii, Percomorpha; Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
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PROSITE; PS50835; IG_LIE; 1.
Immunoglobulin domain; Receptor; Repeat; Transmembrane.
SEQUENCE 394 AA; 44022 MW; EE60B16FA2C2896C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                         394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class I helical cytokine receptor number 1.
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MSIKLYDQWRVWLQKSHKTRNQVL 384
                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                     LSFRLYDQWRAWMQKSHKTRNQVL
                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                         QGUAQS_TETNG PRELIMINARY;
QGUAQS;
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Maucell E., Bouneau L., Flacher C., Ozouf-Costaz C., Bernot A.,
Adillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
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Mincker P., Lander E. S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
"The early vertebrate proto-karyotype.",
                                                                                               120 GETHISTQYTLKYKLRWYGKEKECEDYTHVQPYSCSITRDLHLFTPYEIWVEASNQLGRA 179
                                                                                                                                                                                                                                                                                                                                300 VGNQTSCRLAGLRPGTVYFVQV------GPRRSSASDRIWI-----SDRRV 339
                                                                                                                                                                                                                                                                                                          293 VSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAG----IWSEWSHPTAASTPRSERPG 348
 104 ANLNGSROQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAH 163
                         60 AGINASRQTSGDNLVCHHHKGHILAGSCLYVGMPPAKPVNLTCWSRNTKDLTCSMAPGGR
                                                                                                                                                                                                                                                                    240 SODWKBEKSAPDQERERAWTEPLCILGLRVLMNEKYSVEAGPLQMALLRILLPVLWVMDD
                                                                           GETPLHTNYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSA
                                                                                                                                                     224 RSDVLTLDVLDVVTTDPPPDVHVSRVGCLBDQLSVRWVSPPALKOFLFQAKYQIRYRVED
                                                                                                                                                                                         180 ISDVITLDILDVVTTDPPSGVTVSRVGQLEDQLSVRWEAPPALKDFLFQAKYQIRYRLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF6801, whole genome shotgun sequence.
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Pred. No. 4.6e-29;
7; Mismatches 21; Indels 81.
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Q4TCM7;
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maucell E. Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Maucell E. Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Micalla G., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Parra G., Lardier G., Chaple C., Poulain V., Gouzy J., Parra G., Lardier G., Chaple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindbad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lindet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Waissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
CWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLA
                   LKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSK
                                                                                                                                                                                                                             KAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAY-CS
                                                                         LFTPYEIWVEATURLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope, Whitehead Institute Centre for Genome Research, Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 10 SCAP15019, whole genome shotgun sequence.
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                                                                                                                                                                                                                                                                                                          385 NLSFRLYDQWRAWMQKSHKTRNQV 408
                                                                                                                                                                                                                                                                                                                              SMSMKLYDQWRVLMQKSHKARNQV 389
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ORFNames=GSTENG00031935001;
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Q4RMPS;
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Best Local Simil
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Maturid S., Jaffe D., Fisher S., Iutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Beraddinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
"The early vertebrate proto-karyotype.";
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   288
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                                                                                                                                                                                                                                                                     RLAGLKPGTVY--------FVQVRCNPFGIYGSKKAGIWSEWSHPT 337
                                         ELSRILINTSTILALALANINGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWS
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   231 DVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWK--
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Bukaryota, Metazoi, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha; Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae; Tetraodon.

NCBI_TaxID=99883;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF15947, whole genome shotgun sequence.
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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58.0%; Pred. No. 4.6e-25;
tive 15; Mismatches 37;
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236 VITDPPPDVHYSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Maucell E., Bouneau L., Fischer C., Czouf-Costaz C., Bernot A., Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B., Dasilva C., Salanoubat M. Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruander C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lindet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              OKENAMES=6STENGO0037750001;
Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha
                                                                                                                                                                                                                                                                              13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAPI5948, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 QTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SVLWTVHFVQVRCNPVGIYGSRKAGIWSDWSHPAAASTPNS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 380; DB 2; Length 199; Pred. No. 4.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope, Whitehead Institute Centre for Genome Research, Submitted (FBB-2004) to the EMBL/GenBank/DBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 AA; 21734 MW; 299786CDFB24BDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAE01015948; CAG13473.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           918 AA
                                                                                                                                                                                                                       199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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                                                                                                                                                                                                                       PRT;
                             134 RNTKDLSCRWRPGGLGET 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.9%;
67.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein 130 precursor.
Name=gp130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9W6U9 CHICK PRELIMINARY;
Q9W6U9;
                                                                                                                                                                                                                    Q4RDQ9 TETNG PRELIMINARY;
Q4RDQ9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 67.0
les 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                         RESULT
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151 PINYTLSH--RWAHFGANYCRGANNSC-----TIHSP-GFQFYIDTTFQVEATNEL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 SRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 PVKTQDWEMVPEEDTASHRDSFTLQDLLPNTVYEVSIRC----IHKDGHGFWSDWSELK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 VEDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPT 337
                                                                                                                                                                                                                                          Chen J., Grace A., Chien K.R.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-!- DOWAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).

-!- DOWAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).

EMBL: AF041845; AAC03531.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 DPTLLIGS-SLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 LNSPLTCNVWASGHVANTLYGIFFTLGLPPDKPTNLTCIVYNQDNLTCTWDPGR--PTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 DPGIVHGERPFTAYCVINOTCLREDASRIYWLVKGVKVPETQYEILNOTISSVTFENLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HINYSLKYKLRW-----YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR
                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Repeat; Transmembrane. Sequence 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Prolactin receptor delta 7/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00041; fin3; 4.
Pfam; PF06128; Lep receptor_Ig; 1.
SMART; SMO0060; FN3; 4.
PROSITE; PSS0853; FN3; 5.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%; Score 355.5; DB 2 30.5%; Pred. No. 2.8e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOVTP--EAP-----PSRGP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003529; Hemptrecept 1302.
InterPro; IPR010457; Lep_receptor_Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN_III.
                                     laevis (African clawed frog)
                                                                                                                                Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 30.5
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QETD78 HUMAN PRELIMINARY;
                                                                                                                                                                                                 [1] _
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                  NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 RRLPSELSRLIN-----TSTLALALANINGSRQQSGDNLVCHA-RDGSI---LAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 SCLYVGLPPEKPFNISC-----WSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ISVTVGLPPEKPKNLSCIVYLSPKVEMYMN-----CTWNPGRH--TFLDTRFRLKYMWPR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVV---DDVSNQT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 PRNLSVNS-GILPTVLKLSWEN--QISTVVMELKFNİRYRISSDTNWMEVPPEDTASPRT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 LLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHG---DTPGATAEGLYWTLNG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 LNICSFEV-SGGLVQSCGHIIPESPVLALGSNFTALCILNESCLDFGNIYASQIIWKMKN 74
                                                                                                                                                                                                                                                                                                                 on gpi30 cyrokine receptor signaling.
Development 125.4791.4801(1998).
-1- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).
-1- DOMAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).
EMBL; AJ011688; CAB42084.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                       TISSUE-Embryonic heart primary culture;
MEDLINE-99026068; PubMed-9806927;
Geissen M., Heller S., Pennica D., Ernsberger U., Rohrer H.;
"The specification of sympathetic neurotransmitter phenotype depends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 SFSIQGLRPYTEYVFSIRC-----MKEDGVGFWSDWSERQIGVTTED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score 371; DB 2; Length 91 30.2%; Pred. No. 1.7e-20; ive 41; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         918 AA; 102495 MW; FE7625FF3E3613EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50853; FN3; S.
PROSITE; PS01353; HEMATOPO REC_L_F2; UNK
Receptor; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003529; Hemptrecept_1302.
InterPro; IPR010457; Lep_receptor_Ig.
Pfam; PF00041; fn3; 4.
Pfam; PF06528; Lep_receptor_Ig; 1.
SMART; SM00060; FN3; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential
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057519 XENLA
1D 057519;
AC 057519;
DT 01-JUN-1998 (TrEMBLrel. 06,
DT 01-JUN-1998 (TrEMBLrel. 06,
DT 01-MAR-2004 (TrEMBLrel. 26,
DE GP130P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365
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--KPSKGP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09UHJ5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                      Ensembl; ENGC0000113494; Homo sapiens.

Ensembl; ENGC0000113494; Homo sapiens.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:00161020; C:membrane; IEA.

GO; GO:0004892; F:hematopoietin/interferon-class (D200-domain. .; IEA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR003954; FXHR, recept_B/G.

InterPro; IPR003528; Hemptrecept_Pl.

InterPro; IPR003528; Hemptrecept_Pl.

ENGRI; PF00041; Enj; 2.

PROSITE; PS0043; FN3; 2.

PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 LFLNTCLINGQLPPGKPEIFKCRSPNKETPTCWWRPGTDGG--LPTNYSLTYHREGETLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 FKILSLHPGOKYLVQVRCKP-----DHGYWSAWSPATFIQIPSGD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11518703;
Hu Z.Z., Meng J., Dufau M.L.;
"Isolation and characterization of two novel forms of the
prolactin receptor generated by alternative splicing of a
identified exon 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vonderhaar B.K.;
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 AA; 30705 MW; FBB498AB649A078C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.7%; Score 332; DB 2; Best Local Similarity 37.0%; Pred. No. 4.5e-18; Matches 84; Conservative 28; Mismatches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-007-2003 (TrEMBLrel. 25, Last seq
Prolactin receptor short isoform 1b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q96P36 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trott J.F., Hovey R.C., Submitted (SEP-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
TISSUE=Breast tumor;
                                                                                                                                                                                                         Q8TD78; 29-227
                                                                                                                                                                                      P16471; 1BP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=PRLR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        096P36;
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126 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 LPLNTCLINGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72
                                                                                                                                                                                                                                                                                                                                                                 . .; IEA.
J. Biol. Chem. 276:41086-41094 (2001).

-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).

-!- DOMAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).

EMBL: AF416618; AAL23914.1; -; mRNA.

PIR: B59405; B59405.

HSSP: P16471; 1BP3.

SMR: Q96P36; 29-227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prolactin receptor.",
J. Biol. Chem. 274:35461-35468(1999).
J. Biol. Chem. 274:35461-35468(1999).
J. DOMAIN: The WSXWS morif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 NTCERYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20054419; PubMed=10585417; DOI=10.1074/jbc.274.50.35461; Kline J.B., Roehrs H., Clevenger C.V.; "Functional characterization of the intermediate isoform of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is required for JAK interaction and/or
                                                                                                                                                                                                                                                                                                                           GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. GO:0004872; F:receptor activity; IEA.
InterPro; IPR00296; Cytkn recept_B/G.
InterPro; IPR00356; FN III.
InterPro; IPR003528; Hemptrecept_F1.
Ffan; PF00041; fn3; 2.
SMART; SM00060; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.7%; Score 331; DB 2; Length 288; 37.5%; Pred. No. 6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 FKILSLHPGQKYLVQVRCKP-----DHGYWSAWSPATFIQIP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 AA; 32760 MW; B45203EC045EB417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequent 01-OCT-2003 (TrEMBLrel. 25, Last annotat Intermediate prolactin receptor isoform. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50853; FN3; 2.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- DOMAIN: The box 1 motif is required activation (By similarity).

EMBL; AF166329; AAD498B5.1; -; mRNA.
HSSP, P16471; 1BP3.

SRR; Q9UHJS; 29-227.

GO; GO:0009986; C:cell surface; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84; Conservative
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EMBL; AF416619; AAL23915.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 2.
                                      PIR; A59405; A59405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 298
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"Isolation and characterization of two novel forms of the human prolactin receptor generated by alternative splicing of a newly identified exon 11.";
Biol. Chem. 276:41086-41094(2001).
-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurace receptor binding (By similarity).
-!- DOWAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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GO; GO:0042978; F:crnithine decarboxylase activator uccessor GO; GO:004925; F:prolactin receptor activity; NAS.
GO; GO:004935; F:protein homodimerization activity; NAS.
GO; GO:0006916; P:anti-apoptosis; NAS.
GO; GO:0007166; P:call surface receptor linked signal transdu. .;
GO; GO:0007186; P:atcrathon; NAS.
GO; GO:000664; P:steroid biosynthesis; NAS.
GO; GO:000664; P:steroid biosynthesis; NAS.
R GO; GO:0007117; P:transmembrane receptor protein tyrosine kin. .;
R GO; GO:00042977; P:transmembrane receptor protein tyrosine kin. .;
R GO; GO:00042977; P:tronsmembrane receptor protein tyrosine kin. .;
R InterPro; IPR00396; Cytkn recept_B/G.
R InterPro; IPR00396; Cytkn recept_B/G.
R InterPro; IPR00396; FN III.
R Pfam; PF00041; fn3; 2.
           :0042978; F:ornithine decarboxylase activator activity; NAS
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                             349 AA; 39806 MW; 932F200E850CDD27 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.7%; Score 331; DB 2; 37.5%; Pred. No. 7.7e-18;
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PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
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Q96P35;
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SEQUENCE
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126 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
RESP: P16471; 1873.

RESP: P16471; 1873.

RESP: P16471; 1873.

RESP: RESP: P16471; 1873.

RESP: RESP: RESPONDED 1394; Homo sapiens.

RESP: RESP: RESPONDED 1394; Homo sapiens.

RESP: RESP: RESP: RESPONDED 1394; Homo sactivity; ISS.

RESP: RESP: RESPONDED 1394; Homo decarboxylase activator activity; ISS.

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"Identification of a cDNA encoding a long form of prolactin receptor in human hepatoma and breast cancer cells.";
Mol. Endocrinol. 3:1455-1461(1989).
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1 Similarity 37.5%; Pred. No. 8.4e-18;
84; Conservative 27; Mismatches 95; Indels 18;
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NUCLEOTIDE SEQUENCE (ISOFORM 1).
MEDLINE=99182102; PubMed=10084611; DOI=10.1210/jc.84.3.1153;
Hu Z.-Z., Zhuang L., Meng J., Leondires M., Dufau M.L.;
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PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
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MEDLINE=90114212; PubMed=2558309;
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-1- DOMAIN: The box I motif is required for JAK interaction and/or
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MEDLINE=95075462; PubMed=7984244; DOI=10.1038/372478a0;
Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;
"The X-ray structure of a growth hormone-prolactin receptor complex.";
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Note=Soluble isoform that appears specific for the BT-474 breast
cancer cell line;
                                                                                                                                                                                                Kline J.B., Clevenger C.V.; "Characterization of a novel and functional human prolactin receptor isoform (delta-S1 PRLr) containing only one extracellular fibronectin-
"The human prolactin receptor gene structure and alternative promoter utilization: the generic promoter hPIII and a novel human promoter
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MEDILINE=95286597; PubMed=7768908; DOI=10.1074/jbc.270.22.13133;
Fuh G., Walls J.A.;
"Prolactin receptor antagonists that inhibit the growth of breast
cancer cell lines.";
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-!- INTERACTION.
-|- INTERACTION.
-|- INTERACTION.
-|- STATE | P51956 : INTEX.; NDEX.p=1; INTACL=EBI-476182, EBI-476041; P52735 : VAV2; NDEX.p=1; INTACL=EBI-476182, EBI-297549; P52735 : VAV2; NDEX.p=1; INTACL=EBI-476182, EBI-297549; P52735 : ALTERNATIVE PRODUCTS:
-|- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                           Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                      Clin. Endocrinol. Metab. 84:1153-1156(1999).
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IsoId=P16471-2; Sequence=VSP_001720;
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                                                                                                                                            NUCLEOTIDE SEQUENCE (ISOFORM 2)
                                                                                                                                                                         FISSUE=Mammary carcinoma,
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                                                                                                                                                                                                                                                                                         like domain."
                                                            hP (N) ..
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SIMILARITY: Belongs to the type I cytokine receptor family. Type 1

subfamily.

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R MIM; 176761; Targets of the Min thing decarboxylase activator activity; ISS. R GO; GO:0009986; C:cell surface; IDA. GO; GO:00049986; F:ornithine decarboxylase activator activity; ISS. R GO; GO:00042978; F:ornithine decarboxylase activity; NAS. R GO; GO:00042803; F:protein homedimeriation activity; NAS. R GO; GO:0006916; P:anti-apoptosis; NAS. R GO; GO:0007566; P:embryo implantation; TAS. R GO; GO:0007566; P:embryo implantation; TAS. R GO; GO:0007566; P:embryo implantation; TAS. R GO; GO:0007566; P:ercroid biosynthesis; NAS. R GO; GO:000710; P:transmembrane receptor protein tyrosine kin. .; IDA. GO; GO:000717; P:transmembrane receptor protein tyrosine kin. .; IDA. GO; GO:000717; P:transmembrane receptor protein tyrosine kin. .; IDA. GO; GO:000717; P:transmembrane receptor Protein tyrosine kin. .; IDA. GO; GO:0042977; P:tyrosine phosphorylation of JAK2 protein; NAS. R InterPro; IPR002996; Cytkn. recept_B/G.
                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00041; fn3; 2.
PROSITE; PS50853; Fn3; 2.
PROSITE; PS01322; HEMATOPO REC L F1; 1.
3D-structure; Alternative Eplicing; Glycoprotein; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
SIMILARITY: Contains 2 fibronectin type-III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential).
Pibronectin type-III 1.
Pibronectin type-III 2.
WSXWS motif.
Box 1 motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prolactin receptor.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (in isoform 2).
/FTId=VSP 001720.
DF -> AW (in isoform 3)
/FTId=VSP_012620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (in isoform 3).
/FIId=VSP_012621.
                                                                                                       EMBL, M31661; AAA60174.1; -; mRNA.

EMBL, AF091870; AAD32032.1; -; Genomic_DNA.

EMBL, AF091863; AAD32032.1; JOINED; Genomic_DNA.

EMBL, AF091864; AAD32032.1; JOINED; Genomic_DNA.

EMBL, AF091865; AAD32032.1; JOINED; Genomic_DNA.

EMBL, AF091866; AAD32032.1; JOINED; Genomic_DNA.

EMBL, AF091868; AAD32032.1; JOINED; Genomic_DNA.

EMBL, AF091869; AAD32032.1; JOINED; Genomic_DNA.

EMBL, AF091869; AAD32032.1; JOINED; Genomic_DNA.

EMBL, BR349939; AAM533032.1; JOINED; Genomic_DNA.

EMBL, BC059392; AAM533032.1; -; mRNA.
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By similarity.
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                                                                                                                                                                                                                                                                                                       IntAct; Pi6471; -.
Ensembl; ENSG00001113494; Homo sapiens.
HGNC; HGNC:9446; PRLR.
                                                                                                                                                                                                                                                                  EMBL; S78505; AAB34470.1; -; mRNA.
                                                                                                                                                                                                                                                                               PIR; A40144; A40144.
PDB; 1BP3; X-ray; B=25-235
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SIGNAL 1 24
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126 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
                                                                                                                                                                                                                                          244 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 298
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14.7%; Score 331; DB 1; Length 622;
Best Local Similarity 37.5%; Pred. No. 1.6e-17;
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Search completed: April 11, 2006, 02:16:17 Job time : 124.014 secs

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385
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                    Seattle
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LENGTH:
Sequence 12, Appl
Sequence 32, Appl
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1 MPAGRPGPVAQSARRPPRPL.....WRAWMQKSHKTRNQVLPAKL 413
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Sequence 2, 1
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        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-071-224-19
US-09-071-224-18
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US-09-521-335-12
US-09-071-224-4
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Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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US-09-071-224-20
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US-09-071-224-21
US-09-313-942-42
US-10-282-162-24
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SOPTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
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| Sequence 6, Application US/09071224
| Patent No. 6271343
| GENERAL INPORMATION:
| APPLICANT: Look, Si
| APPLICANT: Presenell, Scott R. APPLICANT: Gilbert, Teresa
| APPLICANT: Gilbert, Teresa
| APPLICANT: Robert, Donald C. APPLICANT: Adams, Robyn L. APPLICANT: Lehner, Joyce M. TITLE OF INVENTION: MAMMALIAN ZCYTORS
| NUMBER OF SEQUENCES: 37
| CORRESPONDENCE ADDRESS:
| STREET: Zymogener:
| STREET: Zymogener: Zymogener:
| STREET: Zymogener: Zymo
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REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÿ
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                               318 PFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAELYWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPNISCWSRNWKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI
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CHIPKDLALFTPYEIWVEATURLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS
                                   VRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN
                                                                   240 VRWVSPPALKDFLFQAKYQIRYRVBDSVDWKVVDDVSNQISCRLAGLKFGTVYFVQVRCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 SSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGLYWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.1%; Score 2118.5; DB 2; Length 98.7%; Pred. No. 1e-189; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09012072

Batent No. 6060276

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE: REG 430

CURRENT APPLICATION NUMBER: US/09/012,072

CURRENT PLING DATE: 1998-01-22

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 405
                                                                                                                                                                                                                  360 KKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 396
                                                                                                                                                                                            378 KKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09120601
Patent No. 6207413
GENERAL INFORMATION:
APPLICANT: Masiatkowski, Piotr
TILLE OF INVENTION: No. 6207413e1 Orphan Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYCSNLSFRLYDOWRAWMOKSHKTRNO---VLPA 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 98.7
Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: MOUSE
US-09-012-072-2
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                                                                                                                                                                                                                                                                                           RESULT 3
US-09-012-072-2
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                                                                                                                            1 MPAGGPGPAAQSARRPPRRLSSLWSPLLLCVLGVPQGGSGAHTAVISPQDPTLLIGSSLH 60
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Sequence 13, Application US/09521335

Sequence 13, Application US/09521335

Patent No. 6800460

GENERAL INFORMATION:

APPLICANT: Oppmann, Birgit

APPLICANT: Kastelein, Robert A.

APPLICANT: Bazan, J. Fernando

TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods

FILE REFERENCE: DX0935K

CURRENT APPLICATION NUMBER: US/09/521,335

CURRENT FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SSOFTWARE: PatentIn Ver. 2.0
                                                                                                 1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
                                                                                                                                                                            61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALALANINGSRQQSGDNLVCH
                                                                                                                                                                                                        61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALALANANGSRQOSGDNLVCH
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                           DB 2; Length 425;
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                                                             Indels
                   Score 2197.5; DB 2
Pred. No. 4.4e-197;
3; Mismatches 4;
                       Query Match 97.6%;
Best Local Similarity 97.6%;
Matches 404; Conservative
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Best Local Similarity
Matches 391; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                 238 PPDVHVSRVGGLEDQLSVRMVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 297
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            1 MPAGRRGPAAQSARRPP-PLLPLL--LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLL 57
                                                                                                                                                                                                                                                                                  178 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATWRLGSARSDVLTLDILDVVTTDP
                                                         61 ATCSIHGDTPGATAEGLYWTLAGRRLPSELENTSTLATSTLALALANLAGSRQOSGDNLVCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 LAGLKRGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGE
                                                                                                                                                      121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGBTFLHTNYSLKYKLRW
                                                                                                                                                                                                                                                      181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09071224

Patent No. 6271343

GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Lebner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSRQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
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CITY: Seattle
STATE: WA
COUNTRY: USA
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REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96.
TELECOMMUNICATION: 1NFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 PFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 PKDLALFTPYEIWVEATWRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRW 240
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Sequence 12, Application US/09521335

Sequence 12, Application US/09521335

Sequence 12, Application US/09521335

Sequence 12, Application

Sequence 12, Application

Sequence 12, Application

Applicant: Oppmann, Birgit

APPLICANT: Timan, Jacqueline C.

APPLICANT: Ratelein, Robert A.

APPLICANT: Bazan, J. Fernando

TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods

FILE REPRENCE: DX0935K

CURRENT APPLICATION NUMBER: US/09/521,335

CURRENT FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 13

SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                       21 SSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGLYWT
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94.7%; Pred. No. 2.5e-189;
iive 5; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 AYCSNLSFRLYDQWRAWMQKSHKTRNQ----VLPA 411
                                                                                                                                                                                                                                                                                                                       94.1%; Score 2118.5; DE 98.7%; Pred. No. 1e-189; ive 2; Mismatches
FILE REPERENCE: REG 630
CURRENT APPLICATION NUMBER: US/09/120,601
CURRENT FILING DATE: 1998-07-22
RARLIER APPLICATION NUMBER: 09/012,072
RARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 2
LENGTH: 405
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 98.7
Matches 389; Conservative
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Best Local Similarity 94.7
Matches 391; Conservative
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; ORGANISM: primate
US-09-521-335-12
                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: MOUSE
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; ORGANISM: Homo Sapien
US-09-866-028-32
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                                                                                                                                                                         61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANINGSRQQSGDNLVCH 120
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APPLICANT: Tummas, Daniel
APPLICANT: Tummas, Daniel
APPLICANT: Wood, WAILHIAM
TITLE OF INVENTION: SECRETED AND TRANSMEWBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/866,028
FURRENT FILING DATE: 2001-05-25
Prior application data removed - congult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
                                                                                                                                      1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
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                                                                                              Gaps
                                                                                              20;
                                                                     Length 425;
                                                                                            IndelB
                                                                                              13;
                                                                     Score 2098; DB 2;
Pred. No. 9.1e-188;
                                                                  Query Match
93.2%; Score 2098; Di
Best Local Similarity
91.1%; Pred. No. 9.1e
Matches 391; Conservative 5; Mismatches
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Patent No. 6642360
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Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
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Filvaroff, Ellen
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-071-224-4
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LENGTH: 422
TYPE: PRT
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HITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERRACE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT APPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR FILING DATE: 000-06-25
PRIOR FILING DATE: 06/069,334
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
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                                                                                             1 MPAGREGEVAQSARREPRELSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
                                                                                                                                    61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH
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                                                 Gaps
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Length 422;
                                                   Indels
93.1%; Score 2096; DB 2; 93.7%; Pred. No. 1.4e-187; ive 7; Mismatches 13;
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US-09-944-457-32
Sequence 32, Application US/09944457
Patent No. 6734288
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
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Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
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APPLICANT: Botstein, David
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Goddard, Audrey
                            Best Local Similarity 93.7
Matches 388; Conservative
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FILING DATE: No. 6734289ember 30, 1999
APPLICATION UNMBRR: PCT/US99/28313
FILING DATE: No. 6734288ember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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OR APPLICATION NUMBER: PCT/US98/19330
OR FILING DATE: September 16, 1998
OR FILING DATE: September 16, 1998
OR FILING DATE: December 1, 1998
OR PILING DATE: December 16, 1998
OR APPLICATION NUMBER: 09/216, 021
OR FILING DATE: December 2, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: MARCH 3, 1999
OR APPLICATION NUMBER: 09/254,311
OR PILING DATE: MARCH 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELING DATE: Pebruary 22, 2000
RAPPLICATION NUMBER: PCT/USOU/05841
RAPLICATION NUMBER: PCT/USOU/05841
RAPLICATION NUMBER: PCT/USOU/08439
R FILING DATE: March 30, 2000
R APLICATION NUMBER: PCT/USOU/14042
R FILING DATE: May 22, 2000
R APPLICATION NUMBER: PCT/USOU/20710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
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APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/28409
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APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: PCT/US00/32678
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APPLICATION NUMBER: PCT/US01/06520
                                                                                                                                                                                                                                                                                                                        TELLING DATE: February 9, 1998

RAPPLICATION NUMBER: 60/075,945

RELLING DATE: February 25, 1998

RAPPLICATION NUMBER: 60/112,850

RELLING DATE: December 16, 1998

OR APPLICATION NUMBER: 60/113,296

OR PILING DATE: December 22, 1998

OR PILING DATE: December 22, 1998

OR APPLICATION NUMBER: 60/146,222
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PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 32
LENGTH: 422
TYPE: PRT
CRGNISM: Homo Sapien
US-09-944-457-32
                                                  R FILING DATE: December 16, 1997
R APPLICATION NUMBER: 60/069,702
R FILING DATE: December 16, 1997
R APPLICATION NUMBER: 60/069,870
R FILING DATE: December 17, 1997
R APPLICATION NUMBER: 60/069,873
R FILING DATE: December 17, 1997
R PILING DATE: December 18, 1997
R FILING DATE: December 18, 1997
R FILING DATE: December 18, 1997
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PILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
                                                                                                                                                                                                                                                                                     FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
                                      APPLICATION NUMBER: 60/069,694
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PRIOR
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APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
APPLICANT: Napier, Mary
APPLICANT: Napier, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                         MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
                                                                                                                                        61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH
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                       Gaps
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                     Indela
                     13;
  1.4e-187
                   7; Mismatches
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CURRENT APPLICATION NUMBER: US/09/945,584
CURRENT FILING DATE: 2001-09-26
FRIOR APPLICATION NUMBER: 09/866,028
PRIOR PELING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
  Pred. No.
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APPLICATION NUMBER: 60/069,696
APPLING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,699
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Patent No. 6908993
GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
93.78;
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Gerritsen, Mary
                   Matches 388; Conservative
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APPLICANT: Botstein, David
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Best Local Similarity
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PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/669, 870
PRIOR PILING DATE: December 17, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR PILING DATE: December 17, 1997
PRIOR PILING DATE: December 17, 1997
PRIOR PILING DATE: December 19, 1998
PRIOR PILING DATE: December 19, 1998
PRIOR PILING DATE: PEDLUARY 9, 1998
PRIOR PELING DATE: PEDLUARY 9, 1998
PRIOR PELING DATE: PEDLUARY 9, 1998
PRIOR PILING DATE: December 12, 1998
PRIOR PILING DATE: December 11, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: September 16, 1998
PRIOR PILING DATE: DECEMBER: 60/146, 222
PRIOR PILING DATE: DECEMBER: 16, 1998
PRIOR PILING DATE: DECEMBER: 16, 1999
PRIOR PILING DATE: DECEMBER: 16, 1999
PRIOR PILING DATE: DECEMBER: 16, 1999
PRIOR PILING DATE: DECEMBER: 11, 1999
PRIOR PILING DATE: PEDLUARY 1009
PRIOR PILING DATE: PE
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NUMBER OF SEQ ID NOS: 120
SEQ ID NO 32
LENGTH: 422
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; OKGANISM: Homo Sapien
US-09-945-584-32
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120
                                                                     121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180
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                                                                                                                                                                LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE 360
                                                                                                                                                                                                          57
ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQOSGDNLVCH
                                          181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                     PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                   PSSGPVRRELKQFLGMLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
                                                                                                                                                                                                                                               Sequence 32, Application US/09944944
Patent No. 6929947
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Grimaldi, Christopher
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Gerritsen, Mary
Goddard, Audrey
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Kljavin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
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APPLICANT: Botstein, David
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                                                                                                                                                                                                                                                                                                                                                               Baton, Dan
                                                                                                                                                                                                                                                                                                                      Patent No. 6929947
GENERAL INFORMATION:
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Gaps

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118 ARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 177
                                                                                                                                                                                                                                               PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 300
                                                                                                                                                                                                                                                                                                                                                             PPDVHVSRVGGLEDQLSVR#VSPPALKDFLFQAKYQIRYRVEDSVD#KVVDDVSNQTSCR 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSSGPVRRELKOFLGWLKKHAYCSNLSFRLYDOWRAWMOKSHKTRNO---VLPA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 411
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CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR PILLING DATE: 2001-05-26
PRIOR FILING DATE: 2001-05-26
PRIOR PELING DATE: 2001-05-26
PRIOR PELING DATE: 2001-05-25
PRIOR PELING DATE: 2001-05-27
PRIOR PILLING DATE: December 3, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PILLING DATE: December 11, 1997
PRIOR PILLING DATE: December 11, 1997
PRIOR PILLING DATE: December 12, 1997
PRIOR PILLING DATE: December 12, 1997
PRIOR PILLING DATE: December 16, 1997
PRIOR PILLING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR PILLING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 873
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Ferrara, Napoleone
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APPLICANT: Botstein, David
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Napier, Mary
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OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: 07/10599/12252
OR FILING DATE: JUNE 22, 1999
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: September 15, 1999
OR APPLICATION NUMBER: PCT/US99/28409
OR PILING DATE: No. 692947ember 30, 1999
OR PILING DATE: No. 692947ember 30, 1999
OR PILING DATE: PCT/US99/28313
OR FILING DATE: PCT/US99/28310
OR PILING DATE: DECEMBER: PCT/US99/28310
OR PILING DATE: DECEMBER: PCT/US99/28311
                                               PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/066,017
PRIOR APPLICATION NUMBER: 60/074,400
PRIOR FILING DATE: December 18, 1999
PRIOR FILING DATE: PEDTUATY 9, 1998
PRIOR FILING DATE: PEDTUATY 9, 1998
PRIOR FILING DATE: PEDTUATY 9, 1998
PRIOR PELLON NUMBER: 60/074,086
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR PELLON DATE: PEDTUATY 25, 1998
PRIOR PELLON DATE: PEDTUATY 25, 1998
PRIOR PELLON DATE: PEDTUATY 25, 1998
PRIOR PELLON DATE: PEDTUATY 26, 1998
PRIOR PELLON DATE: PEDTUATY 26, 1998
PRIOR PELLON NUMBER: 60/113,296
PRIOR PELLON NUMBER: 60/146,222
PRIOR PELLON NUMBER: 60/146,222
PRIOR PELLON NUMBER: 60/146,222
PRIOR PELLON NUMBER: 09/216,021
PRIOR PELLON NUMBER: PCT/US99/2801
PRIOR PELLON NUMBER: PCT/US90/0941
PRIOR PELLON NUMBER: PCT/US90/096
PRIOR PELLON NUMBER: PCT/US90/0941
PRIOR PELLON NUMBER: PCT/US90/0941
PRIOR PELLON NUMBER: PCT/US90/09641
PRIOR PELLON NUMBER: PCT/US90/09641
PRIOR PELLON NUMBER: PCT/US90/09641
PRIOR PELLON NUMBER: PCT/US90/09641
PRIOR PELLON DATE: PEDCUATY 20, 2000
PRIOR PELLON NUMBER: PCT/US90/06520
PRIOR PELLON DATE: PEDCUATY 20, 2000
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PRIOR PELLON DATE: PEDCUATY 20, 2001
PRIOR P
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FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/069,873
FILING DATE: December 17, 1997
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Best Local Similarity 93.7
Matches 388; Conservative
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US-09-944-944-32
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241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 300
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                                                                                                                                                                                                                                                                                                                      LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE 360
                                                                                                                                                                                                                                                                                                                                                                        298 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGE 357
                                                                                                                       178 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDP
                                                                                          181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                  PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
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Pred. No. 3.3e-187;
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OPERATING SYSTEM: DOS
SOFTWARE: FastEEG for Windows Version 2.0
CUREBUT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lok, Si
APPLICANT: Presmall, Scott R.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Rosterr, Donald C.
APPLICANT: Rosterr, Donald C.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Zymogenetics
1201 Eastlake Ave East
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REGISTRATION NUMBER: 32,743
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TELEPHONE: 206-442-6627
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93.5%;
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LENGTH: 422 amino acids
TYPE: amino acid
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APPLICATION NUMBER:
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Best Local Similarity
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FRAGMENT TYPE:
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STREET: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: September 1, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 2, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: March 3, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR FILING DATE: NO. 6936254ember 30, 1999
PRIOR PRILING DATE: NO. 6936254ember 30, 1999
PRIOR PRILING DATE: NO. 6936254ember 30, 1999
PRIOR PILING DATE: PECTUSSO/03565
PRIOR APPLICATION NUMBER: PCT/USSO/0414
PRIOR FILING DATE: February 12, 2000
PRIOR APPLICATION NUMBER: PCT/USSO/04414
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: PEDROST 16, 1999
PRIOR FILING DATE: PEDROST 12, 2000
PRIOR APPLICATION NUMBER: PCT/USSO/14042
PRIOR FILING DATE: PEDROST 12, 2000
PRIOR APPLICATION NUMBER: PCT/USSO/14042
PRIOR FILING DATE: PEDROST 12, 2000
PRIOR PELING DATE: PEDROST 12, 2000
PRIOR PELING DATE: PEDROST 12, 2000
PRIOR FILING DATE: PEDROST 12, 2000
PRIOR FILING DATE: PEDROST 12, 2001
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
     R FILING DATE: December 18, 1997
R APPLICATION NUMBER: 60/070,440
R FILING DATE: January 5, 1998
R RELING DATE: FEBRUARY 9, 1998
R APPLICATION NUMBER: 60/074,096
R RILING DATE: FEBRUARY 9, 1998
R APPLICATION NUMBER: 60/075,945
R FILING DATE: FEBRUARY 3, 1998
R APPLICATION NUMBER: 60/075,945
R FILING DATE: FEBRUARY 35, 1998
R APPLICATION NUMBER: 60/075,945
                                                                                                                                                                                                                                                                                    FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
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298 YRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTA 357
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   238 LPSPATPGLSLLVRGKVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKOFLFQAKYQIR 297
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86.7%; Pred. No. 4.9e-180;
ive 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09012072
Patent No. 6060276
GENERAL INFORMATION:
APPLICANT Masiakowski, Piotr
ITILE OF INVENTION: No. 6060276el Orphan Receptors
FILE REFERENCE REG 630
CURRENT APPLICATION NUMBER: US/09/012,072
CURRENT FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                      399 QKSHKTRNQ-------VLPAKL 413
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US-09-120-601-4
; Sequence 4, Application US/09120601
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Best Local Similarity 86.7°
Matches 379; Conservative
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ORGANISM: HUMAN
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US-09-012-072-4
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                                                          61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH
                                                                                                                              PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                           238 PPEVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                    1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
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 13; Indels
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| Patent No. 6207413
| GENERAL INFORMATION:
| APPLICANT: Masiakowski, Piotr
| TITLE OF INVENTION: No. 6207413e1 Orphan Receptors
| FILE REPERENCE: REG 630
| CURRENT APPLICATION NUMBER: US/09/120,601
| CURRENT PILING DATE: 1998-07-22
| EARLIER APPLICATION NUMBER: 09/012,072
| SARLIER PILING DATE: 1998-01-22
| WUMBER OF SEO.ID NOS: 6
| SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 1.2e-185;
5; Mismatches 14;
8; Mismatches
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il Similarity 86.7%;
391; Conservative
387; Conservative
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US-09-120-601-6
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TYPE: PRT
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Best Local S:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Masiatakowski, Piotr
TITLE OF INTERTION: No. 6207413e1 Orphan Receptors
FILE OF INTERTION: NO. 6207413e1 Orphan Receptors
CURRENT APPLICATION NUMBER: US/09/120,601
CURRENT FILING DATE: 1998-07-22
EARLIER PILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 434
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CRGANISM: HUMAN
US-09-120-601-4
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Search completed: April 11, 2006, 02:18:59 Job time : 29.5393 secs us-09-037-657-13.rapbm

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                                                     April 11, 2006, 02:36:34; Search time 96.1152 Seconds (without alignments) 1795.383 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
5.1.7
Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                1867569 segs, 417829326 residues
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 GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                      - protein search, using sw model
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2251
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Sequence

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| Sequence 13, Application US/09037657A
| Patent No. US20020045741A1
| Sequence 13, Application US/09037657A
| Patent No. US20020045741A1
| SERNERAL INPORMATION:
| APPLICANT: Hilton, Douglas J.
| APPLICANT: Farley, Alicon
| APPLICANT: Alexander, Warren
| APPLICANT: Rakar, Steven
| APPLICANT: Maeda, Masateugu
| APPLICANT: Maeda, Masateugu
| APPLICANT: Maeda, Masateugu
| APPLICANT: Nash, Andrew
| TITLE OF INVENTION: BNOODING SAME
| TITLE OF INVENTION NUMBER: US/09/037,657A
| CURRENT PAPLICATION NUMBER: US/09/037,657A
| CURRENT FILING DATE: 1997-09-11
| NUMBER OF SEQ ID NOS: 54
| CORPUMADE: DALLEY VILLE OF TAKER OF T
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100.0%; Pred. No. 5e-166;
ive 0; Mismatches 0;
US-09-943-851A-32
US-09-944-413-32
US-09-944-896-32
US-09-944-929-32
US-09-944-929-32
US-09-944-852-32
US-09-944-864-32
US-09-944-864-32
US-09-944-864-32
US-09-943-780-32
US-09-943-780-32
US-09-943-64-32
US-09-943-64-32
US-10-677-471-32
US-10-677-471-32
US-10-677-669-32
US-10-677-669-32
US-10-677-669-32
US-10-677-669-32
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US-10-677-669-32
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Matches 413; Conservative
    TYPE: PRT
ORGANISM: Unknown
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61 ATCSIHGDTPGATABGLYWTLNGRRLPSBLSRLINTSTLALALANINGSRQQSGDNLVCH 120
241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 300
                                                LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE 360
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                                                                         Gaps
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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Pred. No. 7.3e-162;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,578
FILING DATE: 13-Unn-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                  Jelmberg, Anna C.
Gilbert, Teresa
Foster, Donald C.
Adams, Robyn L.
Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
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MOLECULE TYPE: procein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09880578
Patent No. US20020045733A1
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 97.6%;
Matches 404; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: WA
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US-09-880-578-6
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                                                                                                                                                                                      360
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                                                                                                PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVBDSVDWKVVDDVSNQTSCR 300
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                                                                                                                                                                                      LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES TITLE OF INVENTION: ENCODING SAME FILE REPERENCE. DAVIES COLLISCON CAVE (CIP)
CURRENT APPLICATION NUMBER: US/09/037,657A
CURRENT FILING DATE: 1998-03-10
EARLIER APPLICATION NUMBER: 08/928,720
EARLIER PILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
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US-09-037-657-15
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98.9%; Score 2226.5; DB 3; Length 425;
Best Local Similarity 98.8%; Pred. No. 4.1e-164;
Matches 409; Conservative 2; Mismatches 0; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/09037657A Patent No. US20020045741A1
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APPLICANT: Abang, Jian-Guo
APPLICANT: Alexander, Warren
APPLICANT: Rakar, Steven
APPLICANT: Rabri, Louis
APPLICANT: Robri, Teteno
APPLICANT: Kojima, Teteno
APPLICANT: Maeda, Masatsugu
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APPLICANT: Nicola, Nicos A.
APPLICANT: Farley, Alison
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APPLICANT: Nash, Andrew
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78 YWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLP 137
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                                                           KKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 13, Application US/1077789; Publication No. US20050048625A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Oppmann, Birgit
APPLICANT: Timans, Jacqueline C.
APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, J. Fernando
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Best Local Similarity
                                                                                                                                              RESULT 5
US-10-778-002-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10247463

Publication No. US20030082724A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dowling, Lynette M.
APPLICANT: Timans, Jacqueline C.
APPLICANT: Gorman, Daniel M.
APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
TITLE OF INVENTION: Methods
FILE REFERENCE: DX0920
CURRENT APPLICATION NUMBER: US/10/247,463
CURRENT APPLICATION NUMBER: US/02-09-18
FRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ'ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 13
                                                                                                                                301 LAGLKRGTVYFVQVRCNPFGIXGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
                                                                                                       YGQDNTCBEYHTVGPHSCHIPKDLALFTPYBIWVBATNRLGSARSDVLTLDVLDVVTTDP
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81 INGRRIPSELSRILINTSTLALALANINGSRQQSGDNLVCHARDGSILAGSCLXVGLPPEK 140
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                                                                                                                                                                 78 YWTLNGRRLPSELSRLLNTSTLALALANINGSRQQSGDNLVCHARDGSILAGSCLYVGLP
                                                                                                                                                                                                  138 PEKPPNISCWSRNMKDLTCRWTPGAHGETPLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS
                                                                                                 CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS
                                                                        18 RPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGL
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Publication No. US20030228653A1
Publication No. US20030228653A1
GENERAL INFORMATION:
APPLICANT: Masiakowski, Piotr
TITLE OF INVENTION:
FILE REFERENCE: REG 630
CURRENT APPLICATION NUMBER: US/09/736,842
CURRENT FILING DATE: 2000-12-14
CURRENT FILING DATE: 1998-07-22
PRIOR PILING DATE: 1998-07-22
PRIOR PILING DATE: RABLIER PILING DATE: 1998-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 405;
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Pred. No. 8.5e-156;
2; Mismatches 0;
    98.5%;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
                             391; Conservative
         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRMVSPPALKDPLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 197
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| Publication No. US20050106673A1
| GENERAL INFORMATION:
| APPLICANT: Dowling, Lynette M. |
| APPLICANT: Dowling, Jacqueline C. |
| APPLICANT: Timans, Jacqueline C. |
| APPLICANT: Garman, Daniel M. |
| APPLICANT: Rastelein, Robert A. |
| APPLICANT: Bazan, J. Fernando |
| TITLE OF INVENTION: Methods |
| TITLE OF INVENTION: Methods |
| TITLE OF INVENTION: Methods |
| FILE REFERENCE: DX0992Q |
| CURRENT FILING DATE: 2004-12-17 |
| PRIOR FILING DATE: 2004-12-17 |
| PRIOR FILING DATE: 2000-05-31 |
| NUMBER OF SEQ ID NOS: 13 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEG ID NOS 5 |
| TENGENT APPLICATION OF 5 |
| SEG ID NOS 5 |
| SEG ID N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 VRWYSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN
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            Methods
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  TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and FILE REFERENCE: DX0935K
CURRENT APPLICATION NUMBER: US/10/777,789
CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: US/09/521,335
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 407
                                                                                                                                                                                                                                                                                                                                                  Length 407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
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Pred. No. 8.5e-156;
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Best Local Similarity 98.5%;
Matches 391; Conservative
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US-11-016-106-5
                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: rodent
US-10-777-789-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-11-016-106-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/10778002

Publication No. US20040192891A1

GENERAL INPORMATION:

APPLICANT: Oppmann, Birgit

APPLICANT: Timans, Jacqueline C.

APPLICANT: Bazan, J. Fernando

TITLE OF INVENTION: Mamalian Cytokines; Related Reagents and Methods

FILE REFERENCE: DX0935K

CURRENT PELING DATE: 2004-02-11,

PRIOR APPLICATION NUMBER: US/10/778,002

CURRENT FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: US/09/521,335

PRIOR APPLICATION NUMBER: US/09/521,335

PRIOR APPLICATION NUMBER: US/09/521,335

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12

LENGTH: 410

TYPE: PRT

CREANISM: primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPAGRRGPAAQSARRPP-PLLPLL--LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
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APPLICANT: Timans, Jacqueline C.
APPLICANT: Gorman, Daniel M.
APPLICANT: Gorman, Daniel M.
APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
TITLE REFERENCE: DX092Q
CURRENT APPLICATION NUMBER: US/10/247,463
CURRENT FILING DATE: 2002-09-18
PRIOR FPLING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent IN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPAKL 413
                                                                                                                                                                                                                                                                                                                                                                                                                           4; Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
93.9%; Score 2114.5; DB 4; Length
Best Local Similarity 94.7%; Pred. No. 1.9e-155;
Matches 391; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                       i LENGTH: 410
; TYPE: PRT
; ORGANISM: primate
US-10-247-463-4
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US-10-778-002-12
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                  301 IYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKH 360
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                                                                                                        321 IYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKH 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 INGRRIPSELSRLINTSTLALALANINGSROOSGDNLVCHARDGSILAGSCLYVGLPPEK 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFG 320
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Fublication No. US20020164785A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/074,901
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: US/09/012,072
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
LENGTH 405
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98.7%; Pred. No. 9.2e-156;
iive 2; Mismatches 0;
                                                                                                                                                                                                                          361 AYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 394
                                                                                                                                                                                            381 AYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYCSNLSFRLYDQWRAWMQKSHKTRNQ----VLPA 411
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; Sequence 4, Application US/10247463
; Publication No. US20030082734A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Lynette M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 98.7
Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: MOUSE
US-10-074-901-2
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US-10-074-901-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180
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                                                                                                                                                 1 MPAGRRGPAAQSARRPP-PLLPLI--LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLL 57
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                      Sequence 4, Application US/11016106

Sequence 4, Application US/11016106

Publication No. US20050106673A1

GENERAL INFORMATION:

APPLICANT: Dowling, Lynette M.

APPLICANT: Timans, Jacqueline C.

APPLICANT: Gorman, Daniel M.

APPLICANT: Garman, Daniel M.

APPLICANT: Bazan, J. Fernando

TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and

TITLE OF INVENTION: Methods

FILE REFERENCE: DX09920

CURRENT APPLICATION NUMBER: US/11/016,106

CURRENT FILING DATE: 2004-12-17

PRIOR APPLICATION NUMBER: PRIROR APPLICATION NUMBER: US/09/588,113

PRIOR FILING DATE: 2000-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSSGPVRRELKOPLGWLKKGHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPAKL 413
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Pred. No. 1.9e-155;
5; Mismatches 14; Indels
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Best Local Similarity 94.7%;
Matches 391; Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: primate US-11-016-106-4
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LENGTH: 410
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                                                                                                                 1 MPAGRRGPAAQSARRPP-PLLPLL--LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/1077789

Publication No. US20050048625A1

GENERAL INFORMATION:

APPLICANT: Oppmann, Birgit

APPLICANT: Timans, Jacqueline C.

APPLICANT: Timans, Jacqueline C.

APPLICANT: Rastelein, Robert A.

APPLICANT: Brand J. Fernando

TITLE REFERENCE: DX0935X

TITLE REFERENCE: DX0935X

CURRENT APPLICATION NUMBER: US/10/777,789

CURRENT FILING DATE: 2004-02-11

PRIOR PPLICATION DATE: 2004-02-11

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 13

SOFTWARE PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                            YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
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                                                                                        1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
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                         Score 2114.5; DB 4;
Pred. No. 1.9e-155;
5; Mismatches 14;
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Pred. No. 1.9e-155;
5; Mismatches 14;
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Best Local Similarity 94.7%;
Matches 391; Conservative
                           Query Match 93.9%;
Best Local Similarity 94.7%;
Matches 391; Conservative
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US-10-777-789-12
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TYPE: PRT
US-10-778-002-12
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JTHER INFORMATION: Description of Unknown Organism: Amino Acid Sequence of NR6
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  177 YGQDNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDP 236
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                                                                              237 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
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                                                      241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                          LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44, Application US/09037657A
Patent No. US20020045741A1
APPLICANT: Hilton, Douglas J.
APPLICANT: Hilton, Douglas J.
APPLICANT: Nicola, Nicos A.
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SEQ ID NO 44
LENGTH: 421
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ORGANISM: Unknown
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358 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPDKL 410
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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DISSEMBLY
SOFTWARE: PASTEMD FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,578
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: «Unknown»
PILING DATE: «Unknown»
ATTONEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32, 743
REGISTRATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                               Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-880-578-4
                                                                                                                                                                                                                             Presnell, Scott R.
Jelmberg, Anna C.
Gilbert, Teresa
Foster, Donald C.
Adams, Robyn L.
                                                                                                                         Sequence 4, Application US/09880578
Patent No. US20020045733A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 425 amino acids
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
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        241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 300

        DD
        237 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 296

        QY
        301 LAGLKPGTVYFVQVRCNPFGTYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE 360

        DD
        297 LAGLKPGTVYFVQVRCNPFGTYGSKKAGIWSEWSHPTAASTPRSERPGPGGACEPRGGE 356

        QY
        361 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411

        DD
        357 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 410
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Search completed: April 11, 2006, 02:43:00 Job time: 97.1152 secs

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April 11, 2006, 02:03:38; Search time 116.124 Seconds (without alignments) 1608.075 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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script	Aaw55012 Novel hae Aay93659 A murine ha Aaw59804 Nucleotid Aay26337 Murine U4 Aay70862 Rat Zcyto Aaw55011 Novel hae Aay29368 Rat Zcyto Aay29780 Murine ha Aay29780 Muse cyt Aab19589 Mouse cyt Adc07180 Mouse cyt Adc07180 Mouse cyt Adc1033 Mouse cyt Adc61033 Mouse cyt Adc61034 Mouse cyt Adc61034 Mouse cyt Adx65015 Mouse cyt Adx61034 Muse np
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	protein; c entry)	; ce euti B002 0002	4 dd D 0>0E030
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The present sequence represents a murine haemopoietin receptor NR6 (CLF-polypeptide. The specification describes a method for the treatment or prophylaxis of disease conditions associated with dysfunctional haemopoietic regulation. The method comprises modulating the production of hemopoietic progenitor cells in a mammal by administration of NR6. Decreasing production of progenitor cells may be used in the treatment of cancer or to induce apoptosis of particular cell types. Increasing production of progenitor cells is used to facilitate postnatal survival in mammals by inducing or promoting suckling. Potential disease conditions may be identified by monitoring NR6 production in postnatal babies or allowing expectant mothers to undergo foetal testing. Low NR6 levels can then be treated immediately
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGAA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine; biologically active complex; haemopoietin receptor; NR6; cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation; differentiation; cell survival; neurotrophic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
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facilitate postnatal survival
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100.0%; Pred. No. 8e-193;
ive 0; Mismatches 0;
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 of hemopoietic progenitor cells and facili
mammals by inducing or promoting suckling
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                                        Claim 5; Page 73-74; 77pp; English
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                                                                                 Gaps
     predisposition to cancers, or for drug screening
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                                                         Length 425;
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                                                          DB 2;
                                                       100.0%; Score 2317; DB 2;
100.0%; Pred. No. 8e-193;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                         The present invention relates to a biologically active complex comprising a haemopoletin receptor, NR6 and cardiotrophin-like cytokine (CLC). The complex is useful in the manufacture of a medicament for the treatment and/or prophylaxis of a subject, as it is involved in facilitating proliferation, differentiation and/or survival of a cell. The components have neurotrophic activity. The present sequence is murine haemopoletin receptor, NR6.2 isoform. The NR6.2 represents the NR6 splice variant obtained due to alternative mRNA splicing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAGLKPGTVYFVQVRCNPPGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
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                                                                                                                                                                                  Hilton DJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 2317; DB 4; Length 425; 100.0%; Pred. No. 8e-193; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                  Bartlett PF,
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                                                                                                                                                                                 Fabri LJ, Reid K,
                                330. .334
/label = WSXWS motif
                                                                                                                                                                                                                                                                                       Claim 26; Page 81-83; 123pp; English
                     Location/Qualifiers
                                                                                                                                                            (AMRA-) AMRAD OPERATIONS PTY LID
                                                                                                        06-OCT-2000; 2000WO-AU001216
                                                                                                                                    12-MAY-2000; 2000AU-00007489
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                                                                                                                                                                                           Наведама М;
                                                                                                                                                                                Jachno KM,
                                                                                                                                                                                                                WPI; 2001-281978/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                          N-PSDB; AAD04193
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 425 AA;
                                                              WO200127157-A1
                                                                                                                            08-OCT-1999;
 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425;
                                                                                                                                                                                                                                                                    of a cell.
                                                                                                                                                                                           Nakata Y,
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                                Domain
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Matches
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This is the amino acid sequence of the murine U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response.

Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, cancer, and allergy)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine, U4 protein; haematopoietin receptor superfamily; cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy.
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Pred. No. 1.8e-192;
); Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the murine U4 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 26-27; 38pp; English.
                                                                                                                                                                                                                    AAW59804 standard; protein; 425 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 424; Conservative
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N-PSDB; AAV41688.
RGPAG 425
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Best Local Similarity
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Gaps

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LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE 360
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                                                                                                                                                                 61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLINTSTLALALANINGSRQQSGDNLVCH
                                                                                                                                                                                   YGODNTCEEYHTVGPHSCHI PXDLALFTPYEIWVEATWRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                                                                                                                                                                                     181 YGÓDNÍCEBYHÍVGPHSCHIPKDLALFÍPYEIWVEATNRLGSARSDVLTLDVLTIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
cardiac pathology; heart enlargement; Zcytor5 ligand.
                                                                                                    1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
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                                         Length 425;
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                                           i, DB 2;
1.8e-192;
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                                                                          0; Mismatches
                                           Score 2313;
Pred. No. 1.0
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97US-00850030.
98US-00023890.
98US-0074721P.
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                                           99.8%;
99.8%;
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                                                                           Matches 424; Conservative
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DC, Adams RL,
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                                                             Similarity
                Sequence 425 AA;
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AAW70862
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                                                                                                                                                                         420
                                                                                                                                                                                                        420
                   240
                                                                                                             360
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                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides and polynucleotides used for treatment of human diseases and disorders e.g. immune disorders or deficiencies caused by fungal, parasitic or viral infections.
                                                                PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                            LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
                                                                                                                                                                         PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine U4 haematopoietin receptor superfamily chain.

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    /label= Putative_signal_sequence

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/label= Mature_murine_U4
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N-PSDB; AAX90752.
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Protein Peptide

Mus sp Key

RESULT 5 AAY26337

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LTD.

DZIEGLEWSKA H

97WO-GB002479, 96AU-00002246, OPERATIONS PTY

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(AMRA-) AMRAD
                                                            11-SEP-1997;
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             WO9811225-A2
                                     19-MAR-1998.
                                                                                                                      (DZIB/)
                                                                                                                                             Hilton
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AAY93658
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                                                                                The present sequence represents a protein designated Zcytors, which is a cytokinin-like receptor. Soluble Zcytors may be administered to downregulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytors could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytors ligands. A probe comprising Zcytors DNA or RNA can be used to determine the presence and integrity of the Zcytors gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytors and therapeutically to modify Zcytors ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 LAGLKRGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420
                                                                                                                                                                                                                                                                                                                                                      61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALALANLNGSROOSGDNLVCH 120
                                                                                                                                                                                                                                                                                                                                                                                                     ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGBTFLHTNYSLKYKLRW 180
                      New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1 in blood
                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening;
                                                                                                                                                                                                                                                                                                      1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
                                                                                                                                                                                                                                                                                                                    MPAGGPGPAAQSARRPPRRLSSLWSPLLLCVLGVPQGGSGAHTAVISPQDPTLLIGSSLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 PSSGPVRRELKQFLGMLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 YGQDNTCEYHTVGPHSCHIPKDLALPTPYBIWVEATNRLGSARSDVLTLDVLDVVTTDP
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                                                                                                                                                                                                                                                         Length 425;
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                                                                                                                                                                                                                                                      98.7%; Score 2288; DB 2; 98.8%; Pred. No. 2.7e-190;
                                                                                                                                                                                                                                                                    Pred. No. 2.7e
1; Mismatches
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                                                         Claim 1; Page 75-76; 55pp; English.
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hes 420; Conservative
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 N-PSDB; AAV70896
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                                                                                                                                                                                                                                                                                                                                                                The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVBDSVDWKVVDDVSNQTSCR
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   3
                                                                                                                                                                                 New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells.
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A, Willson T, Zhang J, Alexander
Maeda M, Kikuchi Y, Nash A;
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98.8%; Pred. No. 5.9e-185;
iive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                      Claim 14; Page 77-81; 182pp; English
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   Hilton DJ, Nicola NA, Farley
Rakar S, Fabri L, Kojima T,
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Matches 409; Conservative
                                                                                           1998-260970/23
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The present invention relates to a biologically active complex comprising a haemopoietin receptor, NR6 and cardiotrophin-like cytchine (CLC). The complex is useful in the manufacture of a medicament for the treatment and/or prophylaxis of a subject, as it is involved in facilitating proliferation, differentiation and/or survival of a cell. The complex or its components have neurotrophic activity. The present sequence is murine haemopoietin receptor, NR6.1 isoform. The NR6.1 represents the NR6 splice variant obtained due to alternative mRNA splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      jically active complex comprising NR6 and cardiotrophin-like-for facilitating proliferation, differentiation and/or survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine; biologically active complex; haemopoietin receptor; NR6; cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation; differentiation; cell survival; neurotrophic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      record issued on 09-SEP-2004 : Correction to Feature Table Key
1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
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                                                                                 361 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
                                                          PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fabri LJ, Reid K, Bartlett PF, Hilton DJ;
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2; Mismatches 0;
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98.8%; Pred. No. 5.9e
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330. .334
/label = WSXWS_motif
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                                                                                                                                                                                                AAE00820 standard; protein; 413
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12-MAY-2000; 2000AU-00007489.
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Matches 409; Conservative
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Unidentified.
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02-JUL-2001
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                      301
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                                                                                                                                                          RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a murine haemopoietin receptor NR6 (CLF-
1) polypeptide. The specification describes a method for the treatment or
prophylaxis of disease conditions associated with dysfunctional
haemopoietic regulation. The method comprises modulating the production
of hemopoietic progenitor cells in a mammal by administration of NR6.
Decreasing production of progenitor cells may be used in the treatment of
cancer or to induce apoptosis of particular cell types. Increasing
production of progenitor cells is used to facilitate postnatal survival
in mammals by inducing or promoting suckling. Potential disease
conditions may be identified by monitoring NR6 production in postnatal
babies or allowing expectant methers to undergo foctal testing. Low NR6
levels can then be treated immediately
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Administering the hemopoietin receptor NR6 is used to modulate production of hemopoietic progenitor cells and facilitate postnatal survival of mammals by inducing or promoting suckling.
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                                                                                                               Haemopoietin receptor NR6; CLF-1; dysfunctional haemopoietic regulation; hemopoietic progenitor cell; cancer; apoptosis; postnatal survival; suckling; postnatal baby; foetal testing.
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Pred. No. 5.9e-185;
2; Mismatches 0; ]
                                                                                   A murine hemopoietin receptor NR6.1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                 WALTER & ELIZA.
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98.8%;
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                                                                                                                                                                                                  Mus musculus
                                            25-SEP-2000
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associated with conditions exhibiting abnormal expression of (R).
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                                                                                                   Sequence 416 AA;
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                                                                   ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW
                      ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLINTSTLALALALANLNGSRQOSGDNLVCH
                                                                                                              YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                              PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                            PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                           LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
                                                                                                                                                                                                         ARDGS I LAGS CLYVGLPPEKPPNI S CWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW
                                                                                                  YGODNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                                                                                                                                                                                                                                                                              DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1; interleukin B30; DSRS1; DCRS1; III-B30; cytokine receptor; diagnosis; inflammatory disorder; inflammatory response; innate immunity; morphogenic development; immunological disorder.
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                                                                                                                                                                                                                                       PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 414
                                                                                                                                                                                                                                                    Kastelein RA;
                                                                                                                                                                                                                                                                                                                                                                                       Mouse DNAX soluble receptor subunit 1.
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                                                                                                                                                                                                                                                                                                                     AAY29780 standard; protein; 416
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            useful as a phosphate labeling enzyme to label substrates, and the subunits DSRS1 and DCRS1 are useful as immunogens for generating antibodies, or as antigens for binding antibodies. Nucleic acids encoding (R) are useful for identifying related DNAs and mRNAs, and variants from other individuals or species. The present sequence represents the specifically claimed mouse DSRS1, for use in the composition of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEKPFNISCWSRNMKDLTCRWTPGAHGETPLHTNYSLKYKLRWYGODNTCERYHTVGPHS 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 VRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN
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                                                                                                                                                                                                                                                                                                                        96.0%; Score 2225; DB 2;
100.0%; Pred. No. 8e-185;
ive 0; Mismatches 0;
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Kastelein RA,

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The present invention describes a composition (I) comprising a recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The PCRS2 polypeptide is useful for binding ligands and for preparing antibodies. The DCRS2 polypeptide is also useful for modulating cell proliferation, for diagnostic and therapeutic applications, for detecting presence of their ligands and in drug screening assays. It is also useful for treating conditions such as immunological disorders. The present sequence represents a cytokine receptor subunit protein which is given in an alignment of various cytokine receptor subunits in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEKPFNISCWSRNMKOLICRWIPGAHGEIFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 197
                                                                                                                                                                                                                                                      Novel composition comprising DNAX cytokine receptor subunit polypeptide useful for regulating immune system function and for treating immunological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2209.5; DB 4
Pred. No. 1.7e-183;
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                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 13-15; 93pp; English.
                                                                                                                                                                                   Gorman DM,
                                                          30-MAY-2000; 2000WO-US014867.
                                                                                                   99US-00322913
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Matches 407; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention
                                                                                                                                                                                   Dowling LM, Timans JC,
                                                                                                                                          (SCHE ) SCHERING CORP
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Best Local Similarity
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                                                                                                                                        The present sequence is that of mouse cytokine-like factor-1 (CLF-1), a cytokine receptor family protein, which forms a complex with human interleukin-B60 (IL-80) (see AAB19586). The IL-B60/CLF-1 cytokine serves as a key physiological factor in motor neuron development and regeneration. A claimed soluble complex comprises at least 6 amino acids of mature IL-60B, at least 6 amino acids of mature IL-60B, at least 6 amino acids of mature chr-1 or at least 6 amino acids of contacting the cell of a cell or tissue culture cell involves contacting the cell with an agonist or antagonist of a complex comprising IL-60B and CLF-1 or CMFF-R. A claimed method of screening for a receptor which binds the complex involves contacting the complex involves contacting the complex involves contacting the complex with a cell expressing the receptor, to form a detectable interation resulting in a physiological response in the cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 RPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNAX cytokine receptor subunit; DCRS2; receptor protein; modulating cell proliferation; diagnosis; detection; drug screening; immunological disorder.
                   Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes, polypeptides, and nucleic acids, useful in research, diagnosis and treating inflammatory and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2209.5; DB 3
Pred. No. 1.7e-183;
0; Mismatches 0;
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                                                                                                     Page 21-22; 97pp; English
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Best Local Similarity 99.8
Matches 407; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 407 AA;
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                                                                                                       Claim 1;
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                                                                                   PPGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWL 377
                                          VRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN
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300 PFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGCVCEPRGGEPSGPVRRELKQFLGWL 359
  180 CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel mammalian cytokines, useful for producing antigen-antibody complex, treating conditions associated with abnormal physiology or development, including inflammatory conditions and/or autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a complex comprising interleukin (IL)-B60, expedientalike factor i (CLF-1) (partner sequence of IL-B60) and CNTF-R (CNTF-receptor). The complex is useful for producing an antigen:antibody complex, useful for treating conditions associated with abnormal physiclogy or development, including inflammatory conditions and/or autoimmune disorders and for generating antibodies which is useful in diagnostic applications. The present sequence is mouse cytokine-like
                                                                       240 VRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN
                                                                                                                                         318 PFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWL
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                                                 VRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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Pred. No. 1.7e-183;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytokine-like factor 1 (CLF-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a composition of matter (I) comprising a substantially pure or recombinant DNAX cytckine receptor subunit 2 (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion protein comprising a DCRS2 sequence. A composition of matter comprises: a comprising a DCRS2 sequence. A composition of matter comprises: a substantially pure or recombinant DCRS2 polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of a fully defined 384 amino acids sequence (SI), given in the specification; a substantially pure or recombinant DCRS2 polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SI; a natural sequence. The purple of a magnist or a magnisting to a mammalian DCRS2 is useful for modulating physiology or development of a call or call culture. Antibodies to a DCRS2 can be used for quantitative detection of interferon. The DCRS2 polypeptides and nucleic acids and their binding agents are potentially useful in treating and disease, especially disease associated with the immune system. This is the amino acid sequence of mouse cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHIPKDLALPTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 YWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLP 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YWTLNGRRLPS-LSRLLMTSTLALALANNGSRQOSGDNLVCHARDGSILAGSCLYVGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition potentially useful for treating immunological disorders, comprises a DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion polypeptide comprising a DCRS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 RPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bazan JF;
                                            DNAX cytokine receptor subunit 2; DCRS2; cell physiology; cell development; cell culture; interferon detection; immune system disorder; NR6; mouse.
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Pred. No. 1.7e-183;
0; Mismatches 0;
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Mouse cytokine receptor subunit NR7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gorman DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.8%;
Matches 407; Conservative 0
                                                                                                                                                                                                                                                                                                                             01-JUN-1999; 99US-0137159P
31-MAY-2000; 2000US-00588113
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GORMAN D M.
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                                                                                                                                                                                      US2003082734-A1.
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(GORM/)
(KAST/)
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Sequence 407 AA;

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197
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                                                                                                                                                                                                          257
                                                                                                                                                                                                                                                 180 CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVJTDPPPDVHVSRVGGLEDQLS 239
                                                                                                                                                                                                                                                                                                                                               317
                                                                                                                                                                                                                                                                                                                                                                                       240 VRWYSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFGIYGSKKAGIWSEWSHPTAASIPRSERPGPGGGVCEPRGGEPSGGPVRRELKQFLGWL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention also provides a method of producing a soluble complex comprising the mature protein portions of IL-B60 and CIR-1 polypeptides. The methods and compositions of the present invention are useful in controlling biology and physiology of mammalian cells, such as cells of mammalian immune system, and in particular for regulating activation, development, differentiation and function of various cell types, including haematopoietic cells. They are specifically useful in treating abnormal medical conditions, including immune disorders, such as I cell immune deficiency, chronic inflammation or tissue rejection, or in cardiovascular or neurophysiological conditions. The present sequence is the mouse cytokine-like factor 1 (CIR-1).
YWTLNGRRLPS-LSRLLNTSTLALALALANINGSRQQSGDNLVCHARDGSILAGSCLYVGLP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFG1YGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated or non-human host cells transfected with expression vectors having nucleic acids encoding cytokines, useful in treating immune disorders, cardiovascular or neurophysiological conditions.
                                                                                                                                                                                                                                                                                                                                               VRWVSPPALKDFLFOAKYOIRYRVEDSVDWKVVDDVSNOTSCRLAGLKPGTVYFVOVRCN
                                                                                                                                                                                                          CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine; interleukin-B60; IL-B60; cell physiology; immune system; haematopoidetic cell; immune disorder; T cell immune deficiency; chronic inflammation; tissue rejection; cardiovascular condition; neurophysiological condition; mouse; cytokine-like factor 1; CLF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to mammalian interleukin-B60 (IL-B60). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGAARGPAG 425
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61 YWTLNGRRLPS-LSRLLANTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLP 119
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                                                                                                                                                                                                PEKPFNISCWSRNMKDLICRWTPGAHGETFLHTNYSLKYKLRWYGODNTCEEYHTVGPHS 197
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                                                                                    1 RPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATABGL
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                                                                  RPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGL
                                  Gaps
                                  1;
Length 407;
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                                  Indels
 DB 8;
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 Score 2209.5; DB 8 Pred. No. 1.7e-183;
                                0; Mismatches
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 95.4%;
 Query Match
Best Local Similarity 99.8
Matches 407; Conservative
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version - 2006
GenCore (c) 1993
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- protein search, using sw model OM protein Run on:

April 11, 2006, 02:10:19; Search time 21.2669 Seconds (without alignments) 1922.808 Million cell updates/sec

US-09-037-657-15 Perfect score:

2317 1 MPAGRPGPVAQSARRPPRPL......NQDEGILPSGRRGAARGPAG 425 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seq seq 08 08 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	BB	ID	scription
-	331	14.3	288	7	B59405	prolactin receptor
7	331	14.3	376	~	A59405	
٣	331	14.3	622	7	A40144	prolactin receptor
4	329	14.2	918	7	A36337	membrane glycoprot
S	319.5	13.8	917	0	149699	glycoprotein 130 -
9	317.5	13.7	918	~	A44257	interleukin-6 sign
7	314	13.6	830	N	I50455	prolactin receptor
60	312	13.5	310	7	A29884	
6	312	13.5	412	~	A41070	
10	312	13.5	610	~	A34631	м
11	312	13.5	610	N	A36116	prolactin receptor
12	307.5	13.3	292	N	177525	prolactin receptor
13	307.5	13.3	303	N	177524	
14	307.5	13.3	909	7	153269	
15	307.5	13.3	616	N	A30304	prolactin receptor
16	306	13.2	831	~	JQ1655	prolactin receptor
17	302.5	13.1	581	~	145971	
18	261.5	11.3	630	N	151086	prolactin receptor
19	254.5	11.0	771	N	B38252	ш
20	254.5	11.0	783	7	JH0329	granulocyte colony
21	254.5	11.0	863	~	C38252	granulocyte colony
22	252.5	10.9	837	7	A34898	granulocyte colony
23	234	10.1	372	~	158141	ciliary neurotroph
24	220.5	9.5	372	Н	UHHUCN	ciliary neurotroph
25	209.5	0.6	422	7	137891	interleukin-11 rec
56	208.5	9.0	432	7	I48343	interleukin-11 rec
27	208	9.0	362	7	S60614	growth promoting a
		8.7	460	7	JL0145	interleukin-6 rece
29	200.5	8.7	468	٦	A41242	interleukin-6 rece

	prolactin receptor	interleukin-6 rece	MPL-K protein prec	MPL-P protein prec	leptin receptor, s	leptin receptor, 8	leptin receptor, s	leptin receptor, 8	leptin receptor, s	lactogen receptor	hematopoietic grow	leukemia inhibitor	leptin receptor, O	proto-oncogene - m	differentiation-st	leptin receptor, i
	A32868	JL0144	B45266	A45266	568441	S68439	568437	S68440	568438	B34631	835317	S17308	PC4184	837622	JX0312	874225
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	126	440	579	635	802	892	894	900	1162	150	625	1097	1162	626	1092	895
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6	T 7 7	194.5	192.5	192.5	191.5	191.5	191.5	191.5	191.5	190	190	190	188.5	186	185	182
ć	3	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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	cells
	cancer
	breast
	lactin receptor short form S1b precursor, breast cancer cells T-
	S1b
	form/
	short
	lactin receptor short form
ULT 1	lactin

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: B59405; B4940
J; Biol. Chem. 276, 41086-41094, 2001
J; Biol. Chem. 276, 41086-41094, 2001
A;Fitle: Isolation and characterization of two novel forms of the human prolactin recep. A;Reference number: A59405; MUID:21538812; PMID:11518703

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-288 <HU1> A;Cross-references: UNIPROT:Q96P36; UNIPARC:UPI00006CDDA; GB:AF214012; PIDN:AF214012.1 R;Hu, Z.Z.

December, 1999 submitted to GenBank,

A;Reference number: A49400 A;Accession: B49400 A;Catus: preliminary A;Molecule type: DNA A;Residues: 1-280 <HUZ>

A;Cross-references: UNIPARC:UP100006CDDA; GB:AF214012; PIDN:AF214012.1 C;Comment: This is one of the short forms (S1a and S1b) of the human proactin receptor ta-casein gene promoter activation, with S1b more effective than S1a. However, their life

A; Gene: GDB: PRLR C, Genetics

A;Cross-references: GDB:120315; OMIM:176761
A;Map position: 5p13.3-5p13.1
C;Keywords: Glycoprotein; transmembrane protein
C;Keywords: Glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-288/Product: prolactin receptor, short form Slb #status predicted <WAT>
F;36-221/Domain: cyrokine receptor homology <CRS>
F;55,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Gaps 18; 14.3%; Score 331; DB 2; Length 288; 37.5%; Pred. No. 3.7e-18; Live 27; Mismatches 95; Indels Query Match 14.3%; Best Local Similarity 37.5%; Matches 84; Conservative

8;

126 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184 185 NTCEEYHTVGPHSCHIPKO-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD ઠ g ઠે

244 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 298 Б ò

299 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342

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Tue Apr 11 10:57:46 2006

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103 LANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGA 162
     A;Residues: 1-622 <BOU>
                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: PRLR
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submitted to GenBank, December, 1999
A.Reference number: A49400
A.Accession: A49400
A.Accession: A49400
A.Status: preliminary
A.Status: preliminary
A.Residues: 1-376 cHU2>
A.Cross-references: UNIPARC:UPI000005B673; GB:AF214012; PIDN:AF214012.1
A.Cross-references: UNIPARC:UPI000005B673; GB:AF214012; PIDN:AF214012.1
C.Comment: This is one of the short forms (Sla and Slb) of the human prolactin receptor cta-casein gene promoter activation, with Sla less effective than Slb. However, their lited COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe
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                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: A59405; A49400
R;Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A;Title: Isolation and characterization of two novel forms of the human prolactin recept A;Reference number: A59405; MUID:21538812; PMID:11518703
                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A59405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <HUI.>
A;Cross-references: UNIPROT:Q96P35; UNIPARC:UPI00006E673; GB:AF214012; PIDN:AF214012.1
R;Hu, Z.Z.
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C; Species: Homo sapiens (man)
C; Species: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C; Accession: A40144; A57018
R; Boutin, J.M.; Edery, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D.; Mol. Endocrinol. 3, 1455-1461, 1989
A; Title: Identification of a cDNA encoding a long form of prolactin receptor in human hareference number: A40144; MUID:90114212; PMID:2558309
A; Molecule type: mRNA
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                                                                                                                                                                      prolactin receptor short form Sla precursor, breast cancer cells T-47D - human
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C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-376/Product: prolactin receptor, short form Sla #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
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     --DHGYWSAWSPATFIQIP 227
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A,Gene: GDB:PRLR
A,Cross-references: GDB:120315; OMIM:176761
191 FKILSLHPGQKYLVQVRCKP--
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Across-references: UNIPROT:P16471; UNIPARC:UP10000132234; GB:M31661; NID:g190361; PIDN: R;Fuh, G.; Wells, J.A.

B.Fuh, G.; Wells, J.A.

J. Biol. Chem. 270, 13133-13137, 1995

A;Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell likeference number: A57018; MUID:95286597; PMID:7768908

A;Reference number: A57018 MUID:95286597; PMID:7768908

A;Recession: A57018

A;Residues: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Residues: 25-228, AM <RES>

A;Cross-references: UNIPARC:UP1000066D208; GB:S78505; NID:g999114; PIDN:AAB34470.1; PID:
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A;Reaidues: 1-918 <HIB>
A;Cross-references: UNIPROT:P40189; UNIPARC:UPI000046B12; GB:M57230; NID:g186353; PIDN
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R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an IL-6 signal transducer, gpl30.
A;Reference number: A36337; MUID:91084844; PMID:2261637
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane glycoprotein gpl10 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 ISPODPTLLIGSSLOATCSIHG---DIPGATAEGLYWTLNGRRLPSELSRLLNTSTLALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: 5p13.3-5p13.1
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-622/Product: prolancin receptor, long form #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
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14.3%; Score 331; DB 2; Length 622
Best Local Similarity 37.5%; Pred. No. 9.7e-18;
Matches 84; Conservative 27; Mismatches 95; Indels
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Local Similarity 28.6%; Pred. No. 2.3e-17;
les 88; Conservative 51; Mismatches 151; Indels
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A;Cross-references: GDB:126725; OMIM:600694
A;Cross-references: GDB:126715; OMIM:600694
A;Map position: Sq115411-5q11
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology <CRS>
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Tue Apr

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rat liver IL-6 signal transducing
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F;36-220/Domain: cytokine receptor homology <CRS1>
F;240-426/Domain: cytokine receptor homology <CRS2>
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C;Species: Columba livia (domestic pigeon)
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150455
R;Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A;Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A;Reference number: 150455; MUID:94283267; PMID:7516866
A;Accession: 150455
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Rattuë norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Dates: 10-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R;Mang, Y.; Neabitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A;Title: Molecular cloning and characterization of the rat liver IL-6 signal
A;Reference number: A44257; MUID:93052397; PMID:1427893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 ISPQDPTLLIGSSLQATCSIHG---DTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 HGETFLHTNYSLKYKLRWYGQD-NTCEEYHTVGPHSCHIPKOLALFTPYBIWVEATNRLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: liver
A; Note: sequence extracted from NCBI backbone (NCBIP:118488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-918 <WAN>
A;Cross-references: UNIPROT:P40190; UNIPARC:UPI000012D4D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.7%; Score 317.5; DB 2; 29.8%; Pred. No. 1.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Mismatches 145;
                                                                                                             interleukin-6 signal transducing molecule gp130 - rat
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13.6%; Score 314; DB 2;
Best Local Similarity 37.1%; Pred. No. 2.9e-16;
Matches 76; Conservative 29; Mismatches 82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keywords: transmembrane protein
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A; Residues: 1-830 < CHE>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 146599; 148370
A;Title: Nolecular Cloning of a murine IL-6 receptor-associated signal transducer, gpl30
A;Title: Molecular Cloning of a murine IL-6 receptor-associated signal transducer, gpl30
A;Title: Molecular Cloning of a murine IL-6 receptor-associated signal transducer, gpl30
A;Title: Molecular Cloning of a murine IL-6 receptor-associated signal transducer, gpl30
A;Reference number: 148370; MUID:92291532; PMID:1602143
A;Status: translated from GB/EMBL/DDBJ
A;Status: references: UNIPROT:000560; UNIPARC:UPI000002845A; GB:M83336; NID:g193591; PIDN:
A;Accession: 148370
A;Accession: 148370
A;Status: translated from GB/EMBL/DDBJ
A;Accession: 148370
A;Status: translated from GB/EMBL/DDBJ
A;Gross-references: UNIPARC:UPI000002845A; EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PI
C;Genetics:
C;Genetics:
A;Gene: gpl30
C;Keywords: gplycoprotein
F;134-314/Domain: cytokine receptor homology <CRS>
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FIDIASIANQLTCNILTFGQLEQNVYGITISGLPPEKPKNLSCIVNEGKKMRCEWDGGR 150
                                                                                                                                                          151 --ETHLETNFTLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGK 206
                                                                                                                                                                                                                                                                           207 VISDHINFDPVYKVKPNPPHILSVINSEELSSILKLIWIN-PSIKSVII-LKYNIQYRIK 264
                                                                                                                                                                                                                                                                                                                                                                                                             265 DASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRC-----MKEDGKGYWSDWSEEASG 319
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                                                                                                      HGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGS 222
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320 IT-YEDRP 326
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Best Local Similarity
Matches 92; Conserv
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lactogen receptor 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Decies: Rattus norvegicus (Norway rat)
C;Date: 13-0ul-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: A34631
R;Zhang, R: Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Bjochem. Biophys. Res. Commun. 168, 415-422, 1990
A;Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
A;Reference number: A34631; MUD:90241201; PMID:2159291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-610 <ZHA>
A; Residues: 1-610 <ZHA>
A; Cross-references: UNIPROT: P05710; UNIPARC: UPI0000170BE1; GB:M34083; NID:g205122; PIDN A; Nore: the authors translated the codon GAG for residue 533 as Gly
F;31-216/Domain: cytokine receptor homology <CRS>
                                                                                                                          A;Cross-references: UNIPARC:UP1000002B19B; EMBL:U07567; NID:g641963; PIDN:AAA61784.1; A;Experimental source: Nb2-11C cell line C;Keywords: transmembrane protein P;31-216/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 TTYECPDYKTSGPNSCFFSKQYTSIWKIXIITVNATNQMGSSSSDPLYVDVTYIVEPEPP 125
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A; Reference number: I55417; MUID: 95014432; PMID: 7929319
                                                                                                                                                                                                                                                            13.5%; Score 312; DB 2;
35.4%; Pred. No. 1.7e-16;
tive 35; Mismatches 85;
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prolactin receptor 2 precursor -
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                           A;Accession: I55417
A;Status: translated from A;Molecule type: mRNA
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Best Local Similarity
Matches 80; Conserv
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Best Local Similarity
Matches 80; Conserv
                                                                                                    A;Residues: 1-412 <RES>
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A,Residues: 1-412 <ALL:
A,Residues: 1-412 <ALL:
A,Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19B; GB:M74152; NID:g206389; PIDN:
R,O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A,Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             projectin receptor precursor - rat
projectins: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A29884
R;Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banville
Cell 53, 69-77, 1988
A;Title: Cloning and expression of the rat prolactin receptor, a member of the growth hc
A;Reference number: A29884
A;Accession: A29884
A;Accession: A29884
A;Accession: A29884
A;Accession: A29884
A;Accession: A29884
A;Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19A; GB:M19304; NID:g206364; PIDN:
C;Keywords: transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-310/Product: prolactin receptor #status predicted <MAT>
F;31-216/Domain: cytokine receptor homology <CRS>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 09-Jul-2004
C;Accession: A41070; 155417
R;Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A;Title: A prolactin-dependent immune cell line (ND2) expresses a mutant form of
A;Reference number: A41070; MUID:92041834; PMID:1718958
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     PPEKPTIIKCRSPEKETFTCWWKPGSDGG---HPTNYTLLYSKEGEERVYECPDYKTAGP
                                                                                                               HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDV--HVSRVGGL
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                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
Mol. Endocrinol. 4, 1136-1143, 1990
A;Attles: Expression of two forms of prolactin receptor in rat ovary and liver.
A;Recession: A36116
A;Recession: A36116
A;Accession: A36116
A;Access
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R;Davis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989
A;Title: Expression of multiple forms of the prolactin receptor in mouse liver.
A;Reference number: 157699; MUD: 89261824; PMID: 2725531
A;Accession: 177525
A;Accession: 177525
A;Accession: 177525
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A;Accession: 177526
A;Cross-references: UNIPROT: O08501; UNIPARC: UPI0000028198; GB:M22959; NID: 9200481; PIDN: F;31-216/Domain: cytokine receptor homology <CRS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 LSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT--CERYHTVGPHSCHIPKD-LAL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 FTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--PP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 ALKDP---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 DKETFICWWNPGSDGG--LPTNYSLIYSKE--GEKNIYECPDYKTSGPNSCFFSKQYISI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSSALAYMLLVLSISLING---QS-----------PPGKPEIHKCRSP 34
Species: Rattus norvegicus (Norway rat)
Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
Accession: A36116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prolactin receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 13.5%; Score 312; DB 2; Similarity 35.4%; Pred. No. 2.8e-16; 80; Conservative 35; Mismatches 85
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13.3%; Score 307.5; Dest Local Similarity 32.6%; Pred, No. 2.5e-Matches 85; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 YGSKKAGIWSEWSHPTAASTP 342
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Best Local Similarity
Matches 80; Conserv
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A;Residues: 1-303 <RES>
A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI00002B197; GB:M22958; NID:g200479; PIDN
F;31-216/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: mRNA
A,Residues: 1-608 <RES>
A,Cross-references: UNIPROT:Q08501; UNIPARC:UPI0000020E90; GB:L14811; NID:g293769; PIDN
R;Moore, N.C.; Oka, T.
Gene 134, 263-265, 1993
A;Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
A;Reference number: JT0671; MUID:94085788; PMID:8262385
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C;Species: Mus musculus (house mouse)
C;Date: 02-Mus-1996 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: IS3269; JT0671; S34356
R;Clarke, D.L.; Linzer, D.I.H.
Endocrinology 133, 224-212, 1993
A;Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
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A; Reacidues: 1-608 + MOO>
A; Cross-references: UNDRRC:UPI0000020ES0; GB:L13593; NID:g347398; PIDN:AAC37641.1;
A; Cross-references: UNDRRC:UPI0000020ES0; GB:L13593; NID:g347398; PIDN:AAC37641.1;
B; Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
submitted to the EMBL Data Library, June 1993
A; Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
A; Reference number: S34356
                                                                                                                                                                                                prolactin receptor precursor - mouse
Cispecies: Mus musculus (house mouse)
Cjacte: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
CjAccession: 177524
Ribavis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989
A;Title: Expression of multiple forms of the prolactin receptor in mouse liver.
A;Reference number: 157699; MUID:89261824; PMID:2725531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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----DHGYWSRWGQBKSIBIP 222
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Matches 85; Conservative
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A;Molecule type: manNA
A;Rolecule type: manNA
A;Rosidues: 1-557,'F', 559-608 <EDE>
A;Cross-references: UNIPARC:UPI0000163824; EMBL:X73372; NID:g312696; PIDN:CAA51789.1; PI
C;Comment: Prolactin receptor have long form and short form which are resulted from alte
C;Comment: This long form receptor is capable of transducing a signal to milk protein ge
C;Reywords: receptor; transmembrane protein
C;Reywords: receptor; transmembrane protein
F;230-253/Domain: cytokine receptor homology <CRS>
F;230-253/Domain: transmembrane #status predicted <TWM>
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                                                                                                                                                                                                                                                                                                                                                                               149
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                                                                                                                                                                                                                      90 LSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSR 149
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                                                                                                                                                                                                                                                                                                    Indels 17; Gaps
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                                                                                                                                                       Length 608;
                                                                                                                                                       Query Match
13.3%; Score 307.5; DB 2; Length
Best Local Similarity 32.6%; Pred. No. 6.2e-16;
Matches 85; Conservative 37; Mismatches 92; Indels
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13.3%; Score 307.5; DB 2;
Best Local Similarity 36.3%; Pred. No. 6.3e-16;
Matches 77; Conservative 28; Mismatches 90;
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SCHI-PKDLALFTPYEIWVEATWRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQ
                                                                                            --LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVY
                                                                                                                                                                                                  FVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                    203 LVOVRCKP-----DHGFWSVWSPESSIQIP 227
                                                                                                   256 LSVRWVS--PPALKDF-
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completed: April 11, 2006, 02:17:25 ne : 22.2669 secs

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April 11, 2006, 02:04:23 ; Search time 126.589 Seconds (without alignments) 2368.694 Million cell updates/sec
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Biocceleration Ltd.
GenCore version
Copyright (c) 1993 - 2006
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1 MPAGRPGPVAQSARRPPRPL......NQDEGILPSGRRGAARGPAG 425 BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-037-657-15 2317 Title: Perfect score: Scoring table: Seguence:

2166443 Total number of hits satisfying chosen parameters:

2166443 seqs, 705528306 residues

Searched:

length: 0 length: 2000000000 seq seq 80 Minimum I Maximum I Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_05.80:*
.: uniprot_sprot:*
: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ption	mus musculu	homo sapien	brachydanio	tetraodon n	gallus gall	xenopus lae	homo sapien	homo sapien		homo sapien	homo sapien	pongo		homo sapien	homo sapien	mus musculu	mus musculu	rattus norv	callithrix	mus musculu	cebus apell	columba liv	rattus norv	rattus norv	mus musculu	mus musculu	oryctolagus				
	Description		075462	Q6dg28	Q6uaq5	Q4 rmp5	Q4tcm7	Q4rdr1	Q4rdq9	6n9w60	057519	Q8td78	096p36	Q9uhj5	Q96p35	P16471	Q5raw0	Q7tq89	Q5fc04	P40189	095000	06pdi9	P40190	Q9n0j7	099jz1	Q865v4	090374	Q58dz7	P05710	Q8c7g1	008501	P14787
	ΙD	CRLF1 MOUSE	CRLF1 HUMAN	Q6DG28 BRARE	Q6UAQ5 TETNG	Q4RMP5 TETNG	Q4TCM7 TETNG	Q4RDR1_TETNG	Q4RDQ9_TETNG	Q9W6U9_CHICK	057519_XENLA	Q8TD78_HUMAN	Q96P36 HUMAN	Q9UHJ5_HUMAN	Q96P35_HUMAN	PRLR_HUMAN	Q5RAWO_PONPY	Q7TQ89_RAT	Q5FC04 HUMAN	ILERB HUMAN	IL6RB_MOUSE	Q6PDI9_MOUSE	IL6RB_RAT		Q99JZ1 MOUSE	Q865V4_CEBAP	PRLR_COLLI	Q58DZ7 RAT	PRLR_RAT	Q8C7G1 MOUSE	PRLR_MOUSE	PRLR_RABIT
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	Length	425	422	389	394	437	207	151	199	918	881	268	288	349	376	622	622	1010	857	918	917	917	918	622	608	622	830	310	610	292	608	616
ه. 10 10	!	100.0	93.9	61.0	59.5	42.9	20.2	18.0	16.4	16.0	15.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.2	14.2	13.8	13.8	•	•	•	13.6	•	13.5	•	13.3	13.3	13.3
	Score	2317	2176.5	1414.5	1378.5	995	468.5	416	380	371	355.5	332	331	331	331	331	m	330.5	329	\sim	319.5	319.5	317.5	316	314.5	314	314	312	312	307.5	307.5	307.5
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Q6jta8 sus scrofa Q7t220 gallus gall Q46561 ovis aries Q04594 gallus gall Q6da0 gallus gall Q91094 meleagris g Q28235 cervus elap Q28172 bos taurus Q9pth9 xenopus lae Q6uap8 tetraodon n Q4sqq8 tetraodon n Q4sqq8 tetraodon n Q6i6f7 eublepharis Q9ibf6 xenopus lae
PRLR PIG Q772Z0 CHICK PRLR SHERP PRLR CHICK G6QDAO CHICK PRLR MELGA PRLR MELGA PRLR PRLR TERRU Q9PTI9 XENLA G6UAPB TETNG Q4SQDB TETNG G616P7 EUBNA Q91BF6 XENLA
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ALIGNMENTS

PHOSPHORYLATION SITE SER-222.

Phosphorylation site SER-222.

Phosphorylation and linear ion trap mass spectrometry.";

Throsphoproteome analysis of mouse liver using immobilized metal

Throsphoproteome analysis of mouse liver using fetal development.";

Throsphorylation system and during fetal development. May be involved in nervous system development (By similarity). Plays an essential role in the initiation and/or maintenance of suckling in neonatal mice.

Throsphorylation sovalently linked di- and tetramers. Forms a heteromeric complex with cardiotrophin-like cytokine (CLC); the CELPI/CLC complex is a ligand for the ciliary neurotrophic factor receptor (CMTPR) (By similarity).

Throsphorylation secreted (By similarity).

Throsphorylation secreted (By similarity).

Throsphorylation secreted (By similarity).

Throsphorylation secreted (By similarity). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. "Suckling defect in mice lacking the soluble haemopoietin receptor factor 1) FUNCTION, AND TISSUE SPECIFICITY.

PUNCTION, AND TISSUE SPECIFICITY.

PubMed=10159701, DOI=10.1016/S0960-9822(99)80266-8;

Alexander W.S., Rakar S., Robb L., Farley A., Willson T.A.,

Zhang J.-G., Hartley L., Kikuchi Y., Kojima T., Nomura H.,

Hasegawa M., Maeda M., Fabri L., Jachno K., Nash A., Metcalf D.,

Nicola N.A., Hilton D.J.;

Nicola N.A., Hilton D.J.; 29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1 Cytokine receptor-like molecule 3) (CRLM-3) (NR6).
Name=Crlf1; Synonyms=Crlm3;
Mus musculus (Mouse). Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. 425 AA PRT; Curr. Biol. 9:605-608(1999). STANDARD; [1] NUCLEOTIDE SEQUENCE. NCBI_TaxID=10090; MOUSE MOUSE CRLF1 N

DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.

SIMILARITY: Belongs to the type I cytokine receptor family. Type 3 ---

subfamily.
SIMILARITY: Contains 2 fibronectin type-III domains. + !

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RGPAG 425
                                                                                                                                      CRLF1 HUMAN
                   421
                                                                                                                  HUMAN
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                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180
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SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
                                                                                                                                                                                                                                                                                                  GOS, GO:0005615; C:extracellular space; TAS.
InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003861; FN III.
InterPro; IPR003110; Ig-like.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 2.
PROSITE; PSS0835; FN3; 2.
PROSITE; PSS0835; GG LIKE; FALSE NEG.
Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
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Pibronectin type-III
Fibronectin type-III
WSXWS motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 2317; DB 1;
; Pred. No. 9.2e-175;
0; Mismatches 0;
                                                                                                                                                                                                                                       HSSP, P40223; 1CD9.
Ensembl; ENSMUSG0000007888; Mus musculus.
MGI; MGI:1340030; Crlf1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
                                                                                                                                                                                                              EMBL; AB040038; BAA92777.1; -; mRNA.
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425; Conservative (
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385
146
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425 AA;
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233
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DISULFID
SEQUENCE
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CARBOHYD
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MUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

Chow B., Chui C., Crowley C., Currell B., Dewel B., Dowd P.,

Rachon J., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Reshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

Nandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

Wood W.L., Goddwaki P.J., Gray A.M.,

Whood W.L., Goddwaki P.J., Gray A.M.,

The secreted protein discovery initiative (SPDI), a large-scale

Tholiformatics assessment.";
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A Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B.B., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,
A Diatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,
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A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Maruy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Heiton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elson G.C.A., Graber P., Losberger C., Herren S., Gretener D., Menoud L.N., Wells T.N.C., Kosco-Vilbols M.H., Gauchat J.-F.; "Cytokine-like factor-1, a novel soluble protein, shares homology with members of the cytokine type I receptor family.";
                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
             075462; Q9UHH5;
29-MAR-2004 (Rel. 43, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1) (CLF-1) (ZcytoR5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Magrangeas F., Jacques Y., Minvielle S., "Cloning and expression of a novel soluble protein containing hematopoietic cytokine receptor domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lok S., Presnell S.R., Jelmberg A.C., Gilbert T., Whitmore Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT, SUBCELLULAR LOCATION, TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                Name=CRLF1; Synonyms=ZCYTOR5; ORFNames=UNQ288/PRO327;
422 AA
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLECTIDE SEQUENCE, SUBUNIT, SUB-
SPECIFICITY, AND INDUCTION.
TISSUE-FEE-al lung;
MEDLINE-98349389; PubMed=9686600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunol. 161:1371-1379(1998)
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    STANDARD;
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0013955; F:cytckine binding; IPI.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
InterPro; IPR002956; Cytkn. recept_B/G.
InterPro; IPR003961; FN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MPAGRRGPAAQSARRPP-PLLPLL--LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ATCSVHGDPPGATABGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 ARDGSILAGSCLYVGLPPEKPVNISCWSKONMKDLTCRWTPGAHGETFLHTNYSLKYKLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 LAGLKRGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 PSSGPVRRELKQPLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANINGSRQQSGDNLVCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGODNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
                                                                                                                                                                                                                                                             Pfam; PF00041; fn3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50835; IG_LIKE; PALSE NEG.
Direct protein sequencing; Disease mutation; Glycoprotein;
Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine receptor-like factor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphoserine (By similarity).
N-linked (GlCNAc. .) (Potenti
N-linked (GlCNAc. .) (Potenti
N-linked (GlCNAc. .) (Potenti
N-linked (GlCNAc. .) (Potenti
N-linked (GlCNAc. .) (Potenti
N-linked (GlCNAc. .) (Potenti
N-linked (GlCNAc. .) (Potenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 By similarity.
195 By similarity.
81 R -> H (IN CISS).
774 L -> R (IN CISS).
774 / FTIG-VAR 017865.
240 D -> B (IN Ref. 3).
745302 MW, AD9DEFCB01B84228 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          Ig-like C2-type.
Pibronectin type-III 1
Pibronectin type-III 2
WSXWS motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2176.5; DB 1
Pred. No. 1.2e-163;
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         Snsembl; ENSG00000006016; Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 402; Conservative
                               HGNC; HGNC:2364; CRLF1.
MIM; 604237; -.
MIM; 272430; -.
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153
195
81
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Best Local Similarity
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CARBOHYD
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DISULPID
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MOTIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fetal lung.

IMDUCTION: Up-regulated in fibroblast primary cell cultures under stimulation by IFN-gamma, ThY-alpha and IL-6.

DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.

BISEASE: Defects in CRLFI are the cause of cold-induced sweating syndrome (CISS) [MIM:272430]. CISS is an autosomal recessive disorder characterized by profuse sweating induced by cool surroundings (temperatures of 7 to 18 degrees Celsius). Additional abnormalities include a high-arched palate, nasal voice, depressed nasal bridge, inability to fully extend the elbows and
  Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  June. J. Hum. Genet. 72:375-383(2003).

-!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory role in the immune system and during feral development. May be involved in nervous system and during feral development. May be involved in nervous system development.

-!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a heteromeric complex with cardiotrophin-like cytokine (CLC); the CRLFI/CLC complex is a ligand for the ciliary neurotrophic factor receptor (CMPTR).

-!- SUBCELLULAR LOCATION: Secreted.
-! TISSUE SPECIPICITY: Highest levels of expression observed in spleen, thymus, lymph node, appendix, bone marrow, stomach, placenta, heart, thyroid and ovary. Strongly expressed also in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22428294; PubMed=12509788; Knappskog P.M., Majewaki J., Livneh A., Nilsen P.T.E., Bringsli J.S., Ott J., Boman H., "Cold-induced sweating syndrome is caused by mutations in the CRLF!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kyphoscoliosis.
SIMILARITY: Belongs to the type I cytokine receptor family. Type
                                                                                                                                                                                                                                                                                                                                                  INTERACTIONS WITH CLC AND CNTFR.
MEDLINE=20423191; PubMed=1096616; DOI=10.1038/78765;
Blon G.C.A., Lelievre E., Guillet C., Chevalier S., Plun-Pavreau Froger J., Suard I., de Coignac A.B., Delneste Y., Bonnefoy J.Y., Gauchat J.-P., Gascan H.;
"CLF associates with CLC to form a functional heteromeric ligand f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 2 fibronectin type-III domains. SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
                                                                                                                                                                                     PROTEIN SEQUENCE OF 38-52.

PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;

"Signal peptide prediction based on analysis of experimentally verified cleavage sites.";

Protein Sci. 13:2819-2824(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA.
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VARIANTS CISS HIS-81 AND ARG-374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurosci. 3:867-872(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the CNTF receptor complex.
Blakesley R.W.,
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Gaps

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14; Indels

DB 1; Length 422;

() (Potential) () (Potential) () (Potential) () (Potential) () (Potential) ()

120

57

240

357

418 RGPA 421

P40223; 1CD9

EMBL; HSSP;

removed.

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PRT;
                                                                                                                                                       361 MSIKLYDQWRVWLQKSHKTRNQ 382
                                                                                                                                         386 LSFRLYDOWRAWMOKSHKTRNQ 407
                                                                                                                                                                                                                         QGUAQS_TETNG PRELIMINARY;
QGUAQS;
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                                                                                                                                                                                               MEDLINE=2238925; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Rapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Rapleton M.J., McKerran K.J., Malek J.A., Gunzatane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., Villalon D.K., Muzny D.W., Sodergen B.J., Lu X., Gibbs R.A., Rhey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anterield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Macherth A., Schein J.B., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 WSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLCVLGVPRGGSGAHTAVISPODPTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Gaps
                                                                                                      ORFNames=zgc:91992;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
61.0%; Score 1414.5; DB 2; Length 389;
Best Local Similarity 68.1%; Pred. No. 2.1e-103;
Matches 260; Conservative 48; Mismatches 67; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43314 MW; E30903B99639864A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                      Last sequence update)
Last annotation update)
                                    389 AA.
                                   PRT;
                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00060, FN3; 2.
PROSITE; PS50853; FN3; 2.
Receptor; Repeat; Transmembrane.
SEQUENCE 389 AA, 43314 MW; E
                                                        25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                               QEDG28_BRARE PRELIMINARY;
QEDG28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                              NCBI_TaxID=7955;
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                                                                                           Zgc:91992.
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c.i. DOMAIN: The WSXWS motif appears to be necessary for protein folial parity).

C.i. DOMAIN: The WSXWS motif appears to be necessary for protein folial man thereby efficient intracellular transport and cellsurface receptor binding (by similarity).

EMBL; AY374473; AAR25664.1; -; mRNA.

EMBL; AY374473; Tetracdon nigroviridis.

GO; GO:0004872; P:receptor activity; IEA.

R InterPro; IPR0012996; Cytkn recept_B/G.

InterPro; IPR0013061; FW III.

R InterPro; IPR00110; Ig-like.

PROSITE; FS00853; FN3; 2.

PROSITE; PS50853; FN3; 2.

PROSITE; PS50853; FN3; 2.
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Which are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also are also a
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                                                                                                                                                                                                                                                                                           244 KDFLFQAKYQIRYRLEESSDWKVVDDVGNQTSCRLAGLRPGTVYFVQVRCNPVGILGSRK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAY-CSN 385
                                                       KDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKK
FIPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPAL
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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59.5%; Score 1378.5; DB 2; Length 394;
Best Local Similarity 67.6%; Pred. No. 1.5e-100;
Matches 259; Conservative 39; Mismatches 80; Indels 5;
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Immunoglobulin domain; Receptor; Repeat; Transmembrane.
SEQUENCE 394 AA; 44022 MW; EE60B16FA2C2896C CRC64;
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Class I helical cytokine receptor number 1.
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Gaps

5

239

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104 ANLNGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAH 163
                                                                                                                                                                                                                                                                                                                                          SODWKBEKSAPDQERERAWTEPLCILGLRVLMNEKYSVEAGPLQMALLRILLPVLWVMDD 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAG----IWSEWSHPTAASTPRSERPG 348
                                                                                                                                     180 TSDVITLDILDVVTTDPPSGVTVSRVGQLEDQLSVRWEAPPALKDFLFQAKYQIRYRLED
                                                                                                          44 AVISPODPTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALAL
                                                                                                                                                                                                                                                                                                             GETFLHTNYSLKYKLRWYGQDNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosteni,
Actinopterygii, Neopterygii, Teleosteni, Buteleosteni, Neoteleosteni,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
       Length 437;
                                                       62; Indels
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Last annotation update)
  ; DB 2;
3.9e-70;
                                                     33; Mismatches
     42.9%; Score 995;
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Nature 431:946-957(2004).
                               Pred. No.
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                             53.8%;
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Q4TCM7;
                                                       Conservative
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13-SEP-2005 (TrEMBLrel.
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                               Similarity
                             Best Local Sim.
Matches 199;
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     Query Match
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Mauceli B., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Eottier P., Coutanceau J.P., Gouzy J.,
Arara G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                             265
                                                                                                                                                                                                                                                       CWSRNTKDLTCSWAPGGRGETHISTQYTLKYKLRWYGKEKECEDYTHVQPYSCSITRDLH 187
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                                                                                                                                                                                                                                                                                                                                     LLLCVLGVPRG-GSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRR
                               LPSELSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSTLAGSCLYVGLPPEKPFNIS
                                                                                                                             CWSRNMKDLICRWIPGAHGETFLHINYSLKYKLRWYGQDNICEEYHTVGPHSCHIPKDLA
                                                                                                                                                                                                                                                                                                       LFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPA
                                                                                                                                                                                                                                                                                                                                                                                                             LKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetraodon nigroviridis (Green puffer).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 10 SCAF15019, whole genome shotgun sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMSMKLYDQWRVLMQKSHKARNQ 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLSFRLYDOWRAWMOKSHKTRNQ 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORFNames=GSTENG00031935001;
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27
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Maucell E. Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Cattolico L., Poulain J., De Berardinis V.,
Anthouard C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Rellis M., volff JN., Guigo R., Zody M.C., Mesirov J.,
Arichia G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A. Hindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                    231 DVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWK-- 288
                                                                                                                                                                                                                             ----FVQVRCNPFGIYGSKKAGIWSEWSHPT 337
                                                                                                                                                                                                                                             ------ 299
                                                                                                                                                                                                   61 KSAFDQERERAWTEPLCILGLRVLMNEKYSVEAGPLQMALLRILLPVLWVMDDVGNQTSC 120
                                                                                                                                               9
                                                                                                                                     Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Meopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF15947, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which is
                                                                                         81;
                                                                Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope, Whitehead Institute Centre for Genome Research, Submitted (FBB-2004) to the EMBL/GenBank/DBJ databases.
-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which preliminary data.

EMBL, CAABIO105947; CAG13471.1; -; Genomic_DNA.

NON TER 151 151
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58.0%; Pred. No. 6.6e-25;
tive 15; Mismatches 37; Indels
                                                                                            Indels
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                                       22607 MW; 71F8E80B9998309F CRC64;
                                                                Score 468.5; DB 2
Pred. No. 6.9e-29;
EMBL; CAAE01006801; CAF89355.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                    338 AASTPRSERP----GPGGGVCEPRGGEPSSG 364
                                                                                                                                                                                                                                                                                                             181 AASTPHSGEPPLPAGPGRSL----GSAPESG 207
                                                                                           7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                151
                                                                 20.2%;
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Q4RDR1;
                                                                                            Matches 102; Conservative
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                         207 2
207 AA;
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Best Local Similarity
Matches 80; Conserv
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Best Local Similarity
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Autillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Iuffalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli E., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chaple C., McKernan K.J., McEwan P., Bosak S.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander B., Weissenbach J., Roest Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
IT the early vertebrate proto-karyotype.",
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                                                                                                                                           89 ELSRILINTSTLALALANINGSROQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWS 148
                                                                                                                                                                                74 STYGRLGPHTLSVTLHNINGSRQQSGDNLVCHSSDGHVLAGACLVVGMPPEKPVNLTCWS 133
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LCVLGVPRGGSGAHTAVISPODPTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPS
                                                20 VCVC----GHHPDVAEVSPQDPVLPIGSSLTATCTLSPEL-RLLSSALYWTLNGETLPS
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Acatinopterygii, Neopterygii, Teleostel; Euteleostel, Neoteleostel,

Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;

Tetradontoidea, Tetraodontidae, Tetraodon.
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Chromosome undetermined SCAF15948, whole genome shotgun sequence.
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1 Similarity 67.0%; Pred. No. 6.6e-22;
73; Conservative 8; Mismatches 14: Tndele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                          149 RNMKDLTCRWTPGAHGET 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 PVKTQDWEMVPERDTASHRDSFTLQDLLPNTVYEVSIRC----IHKDGHGFWSDWSELK 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 VEDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen J., Grace A., Chien K.R.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).
-!- DOMAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).
-EMBL; AF041845; AAC03531.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 DPTLLIGS-SLOATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 DPGIVHGERPFTAYCVINQTCLREDASRIYWLVKGVKVPETQYEIINQTTSSVTFENLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 SRQQSGDNLVCHARDGSILAGSCLYVGLPPBKPFNISCWSRNMKDLTCRWTPGAHGETFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTNYSLKYKLRW-----YGQDNTCEBYHTVGPHSCHIPKDLALFTPYBIWVRATNRL
                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.3%; Score 355.5; DB 2; Length 881; illarity 30.5%; Pred. No. 3.8e-19; Conservative 43; Mismatches 136; Indels 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50853; FN3; 5.
PROSITE; PS01353; HEMATOPO REC_L_F2; UNKNOWN_1.
Receptor; Repeat; Transmembrane.
SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                 881 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AASTPRSERPGPGGGVCEPRGGEPSSGP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 KQVTP--EAP------PSRGP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN III.
InterPro; IPR003529; Hemptracept_1302.
InterPro; IPR010457; Lep_receptor_Ig.
Pfam; PF00341; fn3; 4.
Pf00328; Lep_receptor_Ig; 1.
SMART; SM0060; FN3; 4.
                                                                 PRT;
                                                                                                                               Created)
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                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8TD78_HUMAN PRELIMINARY;
Q8TD78;
                                                          OS7519 XENLA PRELIMINARY;
057519;
                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355
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01-JUN-2002 (
01-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Sig
Matches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221
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Q8TD78 HUM
ID Q8TD7
AC Q8TD7
DT 01-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : || :::| | :::| | 1.4 ETPPDCIPEYVN---NSCTI-SDVQPFVNLEVWVEAANALGKAESDHLVFDPIEIVKPPP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 RRIPSELSRLIN-----TSTLALALANINGSRQQSGDNLVCHA-RDGSI---LAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 SCLYVGLPPEKPFNISC-----WSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ISVTVGLPPEKPKNLSCIVYLSPKVEWYMN-----CTWNPGRH--TFLDTRFRLKYMWPR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 PRNLSVNS-GILPTVLKLSWEN--QISTVVMELKFNIRYRISSDTWWMEVPPEDTASPRT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 LLLCVLGVPRGGSGAHTAVISPODPTLLIGSSLQATCSIHG---DTPGATAEGLYWTLNG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on gpi30 cytokine receptor signaling...)
Development 125:4791-4801(1998).
-!- DOMAIN: The WSXWS motif appear to be necessary for proper protein folding and thereby efficient intracelular transport and cell-surface receptor binding (By similarity).
-!- DOMAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).
EMBL; AJ011688; CAB42084.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVV---DDVSNQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Embryonic heart primary culture;
MEDLINE-99026068; PubMed=980927;
Geiseen M., Heller S., Pennica D., Ernsberger U., Rohrer H.;
"The specification of sympathetic neurotransmitter phenotype depends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : ||:| | : ||:| | 287 SFIQGLRPYTEYTEYFISIRC-----MKEDGVGFWSDWSERQIGVTTED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.0%; Score 371; DB 2; Length 91 Best Local Similarity 30.2%; Pred. No. 2.4e-20; Matches 111; Conservative 41; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     918 AA; 102495 MW; FE7625FF3E3613EF CRC64;
                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50853; FN3; 5.
PROSITE; PS01353; HEMATOPO REC_L_F2; UNKNOWN_1.
Receptor; Repeat; Signal; Transmembrane.
918 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P40189; 1800.
InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003996; FN_III.
InterPro; IPR003529; Hemptrecept_1302.
InterPro; IPR01457; Lep_recept_1302.
Pfam; PF00041; fn3; 4.
SMART; SM00060; FN3; 4.
                                                              Created)
PRT;
                                                       01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26, Glycoprotein 130 precursor.
Q9W6U9 CHICK PRELIMINARY;
                                                                                                                                                                                                                 Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGEPSSGP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --KPSKGP 334
                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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244 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prolactin receptor.";
J. Biol. Chem. 274:35461-35468(1999).
-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 NTCEBYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=2005419; PubMed=10585417; DOI=10.1074/jbc.274.50.35461; Kline J.B., Roehrs H., Clevenger C.V.; "Functional characterization of the intermediate isoform of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P16471; 1BP3.

SMR; Q96P36; 29-227.

SMR; Q96P36; 29-227.

GO; GO:01016020; C:membrane; IEA.

GO; GO:0004895; F:neceptor activity; IEA.

InterPro; IPR002996; Cytkn recept_B/G.

InterPro; IPR003861; FN III.

InterPro; IPR003861; FN III.

FEam; PF00041; fn3; 2.

SMART; SM00060; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 FKILSLHPGQKYLVQVRCKP-----DHGYWSAWSPATFIQIP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 AA; 32760 MW; B45203EC045EB417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O.T.M.Y. 2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Intermediate prolactin receptor isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 331; DB 2; L. Pred. No. 8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSS0853; FN3; 2.
PROSITE; PSO1352; HEMATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UHJ5_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 37.5 tes 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                     NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 NICEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl; ENGGO000113494; Homo sapiens.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016022; C:membrane; IEA.

GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.

GO; GO:0004892; F:receptor activity; IEA.

InterPro; IPR002996; Cytkn recept_B/G.

InterPro; IPR003961; FN_III.

InterPro; IPR003528; HemptreceptL_FI.

Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                TISSUE-Breast tumor;
Trott J.F., Hovey R.C., Koduri S., Vonderhaar B.K.;
Submitted (MMR-2002) to the EMBL/GenBank/DDB databases.
-!- DOMAIN: The WSXWS motif appear intracellular transport and cell-folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).
-!- DOMAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).
EMBL; AF492470; AAM18048.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKILSLHPGQKYLVQVRCKP-----DHGYWSAWSPATFIQIPSGD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 AA; 30705 MW; FBB498AB649A078C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 14.3%; Score 332; DB 2; Similarity 37.0%; Pred. No. 6.1e-18; 84; Conservative 28; Mismatches 97,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
TISSUE=Placenta;
Trott J.F., Hovey R.C., Vonderhaar B.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00060; FN3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS01352; HEWATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last seq 01-OCT-2003 (TrEMBLrel. 25, Last ann Prolactin receptor short isoform lb. Name=PRLR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
        Prolactin receptor delta 7/11.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                        sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .; IDA.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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RGO; GO:0004986; C:cell surface; IDA.
RGO; GO:0042978; F:ornithine decarboxylase activator activity; NAS.
RGO; GO:0042803; F:prolactin receptor activity; NAS.
RGO; GO:00042803; F:prolactin receptor activity; NAS.
RGO; GO:0004516; P:anti-apoptosis; NAS.
RGO; GO:0007166; P:cell surface receptor linked signal transdu. .;
RGO; GO:0007165; P:ateroid biosynthesis; NAS.
RGO; GO:0007107; P:trossmembrane receptor protein tyrosine kin. .;
RGO; GO:000711; P:transmembrane receptor protein tyrosine kin. .;
RGO; GO:0007171; P:transmembrane receptor Protein tyrosine tyrosine tyrosine tyrosine tyrosine tyrosin
folding and thereby efficient intracellular transport and cell-

surface receptor binding (By similarity).
-!- DOMAIN: The box 1 motif is required for JAK interaction and/or

activation (By similarity).
EMBL; AF166329; AAD49855.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                      NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hu Z.Z., Meng J., Dufau M.L.; "Isolation and characterization of two novel forms of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 14.3%; Score 331; DB 2; Length 349; Local Similarity 37.5%; Pred. No. 1e-17; Nes 84; Conservative 27; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vonderhaar B.K.;
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 AA; 39806 MW; 932F200E850CDD27 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Prolactin receptor short isoform la.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trott J.F., Hovey R.C.,
Submitted (SEP-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50853; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
PubMed=11518703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Matches
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244 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 298
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                  Homo sapions (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R GO: 00009986; C:cell surface; ISS.
R GO: 00009986; C:cell surface; ISS.
R GO: 000042978; F:ornithine decarboxylase activator activity; ISS.
R GO: 000042978; F:protein neceptor activity; ISS.
R GO: 00006916; P:anti-apoptosis; ISS.
R GO: 00006916; P:anti-apoptosis; ISS.
R GO: 00007595; P:protein homodimerization activity; ISS.
R GO: 000077595; P:actil surface receptor linked signal transdu. . ; IER
R GO: 000077595; P:lactation; ISS.
R GO: 00006694; P:steroid biosynthesis; ISS.
R GO: 00006694; P:steroid biosynthesis; ISS.
R GO: 00006694; P:steroid biosynthesis; ISS.
R GO: 000042171; P:transmembrane receptor protein tyrosine kin. . ; IER
R GO: 000042977; P:tyrosine phosphorylation of JAK2 protein; ISS.
R InterPro; IPR00396; Cytkn recept_B/G.
R InterPro; IPR00358; Hemptrecept_B/G.
R InterPro; IPR00358; Hemptrecept_F.
R SMART; SM00606; FN3: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD
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MEDLINE=90114212; PubMed=2558309;
Boutin J.-M., Edery M., Shirota M., Jolicoeur C., Lesueur L., Ali S.,
prolactin receptor generated by alternative splicing of a newly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 FKILSLHPGQKYLVQVRCKP-----DHGYWSAWSPATFIQIP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 376 AA; 42639 MW; 112DC2555FBC4601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%; Score 331; DB 2; 37.5%; Pred. No. 1.1e-17; ive 27; Mismatches 95
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Prolactin receptor precursor (PRL-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
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                                                                                                                                                                                                                                                                                                                                                       Ensembl; ENSG0000113494; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50853; FN3; 2.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 37.5%
Matches 84; Conservative
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                                                                                                                                                                                                                                                                                                HSSP; P16471; 1BP3
SMR; Q96P35; 29-22
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Controller, Problem 12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strauser R.D., Colline F.S., Wagner L., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Dicthenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C., Rapleton M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Raba S.S., McKernan R.J., McKernan R.J., McKernan R.J., Walke J.A., Gunaratne P.H., Richards S., Worley K., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakebley R.W., Touchman J.W., Green E.D., Dickson M.C., Antiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzyninski M.I., Skalska U., Smailus D.E., McHertfield Y.S.N., Krzyninski M.I., Skalska U., Smailus D.E., McHertfield M., Schehr J.E., Jones S.J.M., Marra M.A., Schehr J.E., Grone E.D., Dickson M.A., Schehr J.E., Jones S.J.M., Marra M.A., Schehr J.E., Jones S.J.M., Marra M.A., Schehr J.E., Jones S.J.M., Marra M.A., Schehr J.E., Jones S.J.M., Marra M.A., Schehr J.E., Jones S.J.M., Marra M.A., Schehr J.E., Jones S.J.M., Marra M.A., Schehr J.E., Jones S.J.M., Marra M.A., Schehr J.E., Jones S.J.M., Marra M.A., Schehr J.E., Jones S.J.M., Marra M.A., Schehr J.E., Jones E.D., Jones R.D., Jones L.D., Jones J.M., Marra M.A., Schehr J.E., Jones S.J.M., Marra M.A., Schehr J.E., Jones E.D., Jones L.D., Jones L.D., Jones J.M., Marra M.A., Schehr J.E., Jones E.D., Jones L.D., Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.
MEDLINE=95075462; PubMed=7984244; DOI=10.1038/372478a0;
Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;
"The X-ray structure of a growth hormone-prolactin receptor complex.";
Nature 372.478-481(1994).
-1-FUNCTION: This is a receptor for the anterior pituitary hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isold=P16471-3; Sequence-VSP 012620, VSP 012621;
Note-Soluble isoform that appears specific for the BT-474 breast
                                                                                                                                                                                                                                                  NUCLECTIDE SEQUENCE (ISOFORM 2).
TISSUE=Mammary carcinoma;
Kline J.B., Clevenger C.V.;
"Characterization of a novel and functional human prolactin receptor "Characterization of a novel and functional human prolactin receptor isoform (delta-S1 PRLr) containing only one extracellular fibronectin-
                                                                                            NUCLEOTIDE SEQUENCE (ISOFORM 1).
MEDLINE=99182102; PubMed=10084611; DOI=10.1210/jc.84.3.1153;
HU Z.-Z., Zhuang L., Meng J., Leondires M., Dufau M.L.; Inche human prolactin receptor gene structure and alternative promoter utilization: the generic promoter hPIII and a novel human promoter
Gould D., Djiane J., Kelly P.A.;
"Identification of a cDNA encoding a long form of prolactin receptor in human hepatoma and breast cancer cells.";
Mol. Endocrinol. 3:1455-1461(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fuh G., Wells J.A.; "Prolactin receptor antagonists that inhibit the growth of breast cancer cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Mammary carcinoma;
MEDLINE=95286597; PubMed=7768908; DOI=10.1074/jbc.270.22.13133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P51956:NEK3; NDExp=1; IntAct=EBI-476182, EBI-476041; P52735:NAV2; NDExp=1; IntAct=EBI-476182, EBI-297549; -1- SUBCELLILAR LOCAFION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                      NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                       (N) .";
Clin. Endocrinol. Metab. 84:1153-1156(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=2; Synonyms=Delta-S1;
IsoId=P16471-2; Sequence=VSP_001720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P16471-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 270:13133-13137(1995).
[6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - 1 - INTERACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prolactin.
                                                                                                                                                                                                                                                                                                                                                       like domain.
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A GO; GO:0009986; C:cell surface; IDA.

GO; GO:0009986; C:cell surface; IDA.

GO; GO:00042978; F:cornithine decarboxylase activator activity; ISS.

GO; GO:00042803; F:protein homodimentation activity; NAS.

R GO; GO:0006916; P:anti-apoptos18; NAS.

GO; GO:0007566; P:enbryo implantation; TAS.

GO; GO:0007566; P:embryo implantation; TAS.

R GO; GO:0007566; P:embryo implantation; TAS.

R GO; GO:0007567; P:lactation; NAS.

R GO; GO:0007710; P:transmembrane receptor protein tyrosine kin. .; IDA.

GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.

GO; GO:0007171; P:transmembrane receptor protein; NAS.

R GO; GO:0007171; P:transmembrane receptor protein; NAS.

R GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.

GO; GO:0007171; P:transmembrane receptor protein; NAS.

R InterPro; IPR0029961; FN III.

R InterPro; IPR0039518; Hemptreceptor FI.
                                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
               DOWAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.
                                                                                                                                           -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50853; FN3; 2.
PROSITE; PS01352; HEWATOPO_REC_L_F1; 1.
3D-structure; Alternative Splicing; Glycoprotein; Receptor; Repeat;
                                                                                         DOMAIN: The box 1 motif is required for JAK interaction and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Box I motif.
N-linked (GLNAc. .) (Potential).
N-linked (GLNAc. .) (Potential).
N-linked (GLNAc. .) (Potential).
                                                                                                                                                                                                  SIMILARITY: Contains 2 fibronectin type-III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prolactin receptor.
Extracellular (Potential)
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/FTId=VSP 001720.
DF -> AW (in isoform 3)
/FTId=VSP 012620.
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                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF091870; AAD32032.1; -; Genomic_DNA.

EMBL; AF091863; AAD32032.1; JOINED; Genomic_DNA.

EMBL; AF091864; AAD32032.1; JOINED; Genomic_DNA.

EMBL; AF091866; AAD32032.1; JOINED; Genomic_DNA.

EMBL; AF091866; AAD32032.1; JOINED; Genomic_DNA.

EMBL; AF091866; AAD32032.1; JOINED; Genomic_DNA.

EMBL; AF091868; AAD32032.1; JOINED; Genomic_DNA.

EMBL; AF091869; AAD32032.1; JOINED; Genomic_DNA.

EMBL; AF091869; AAD32032.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity.
By similarity.
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Ensembl; ENSG00000113494; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF349939; AAK32703.1; -; mRNA.
EMBL; BC059392; AAH59392.1; -; mRNA.
EMBL; S78505; AAB34470.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M31661; AAA60174.1; -; mRNA.
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SIGNAL 1 24
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14.3%; Score 331; DB 1; Length 622;
Best Local Similarity 37.5%; Pred. No. 2.1e-17;
Matches 84; Conservative 27; Mismatches 95; Indels
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Search completed: April 11, 2006, 02:16:16 Job time : 127.589 secs

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SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
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TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: SINGle
TOPOLOGY: linear
MOLECULE TYPE: protein
PRAGMENT TYPE: internal
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                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: WA
COUNTRY:
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US-09-071-224-6
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April 11, 2006, 02:16:39; Search time 29.3685 Seconds (without alignments) 1196.422 Million cell updates/sec
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       GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-866-028-32
US-09-944-457-32
US-09-944-584-32
US-09-945-587-32
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US-09-521-335-12
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Maximum Match 100%
Listing first 45 summaries
                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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US-09-313-942-21
US-09-313-942-10
US-10-282-162-10
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASESEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
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Sequence 6, Application US/09071224

Patent No. 6271343

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Presnell, Scott R.

APPLICANT: Gilbert, Teresa

APPLICANT: Foster, Donald C.

APPLICANT: Adams, Robyn L.

APPLICANT: Lehner, Joyce M.

TITLE OF INVENTION: Madmalian ZCYTOR5

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenet'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFRENCE/DOCKET NUMBER: 96-2:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
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241 VSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKRGTVYFVQVRCNPFG 300
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PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 179
                                                                                                                      240 VRWYSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN 299
                                                                                                                                                                       PFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWL 377
                                                                                                                                                                                           180 CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLS
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                                                                                                      VRWVSPPALKDPLPQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCN
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Best Local Similarity 100.0%; Pred. No. 5.1e-198;
Matches 405; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  6060276el Orphan Receptors
                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09012072;
Patent No. 6060276;
GENERAL INFORMATION:
APPLICANT: Masiakowski, Piotr
ITLE OF INVENTION: No. 6060276e1 Orphan Rec;
FILE REFERENCE: REG 630
CURRENT APPLICATION NUMBER: US/09/012,072;
CURRENT FILING DATE: 1998-01-22;
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
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US-09-120-601-2
; Sequence 2, Application US/09120601
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ORGANISM: MOUSE
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US-09-012-072-2
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                                                                                                                                                                                                                                                                                                                                240
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                                                                                                                                                        ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH 120
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Patent No. 6800460
GENERAL INFORMATION:
GENERAL INFORMATION:
BAPLICANT: COPMEN, Birgit
APPLICANT: Timans, Jacqueline C.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
FILE REFERENCE: DX0935X
CURRENT APPLICATION NUMBER: US/09/521,335
CURRENT FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 13
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                     Length 425;
                                                     Indels
                                                         4
                   Score 2288; DB 2;
Pred. No. 2.3e-205;
1; Mismatches 4;
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Best Local Similarity 99.8%;
Matches 407; Conservative (
                 Query Match 98.7%;
Best Local Similarity 98.8%;
Matches 420; Conservative
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US-09-521-335-13
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US-09-521-335-13
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58 ATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANINGSRQRSGDNLVCH 117
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC:
CURRENT APPLICATION NUMBER: US/09/944,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGODNICEBYHTVGPHSCHIPKDLALFIPYEIWVEATURLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                               DB 2; Length 422;
        FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
                                                                                                                                                                                                                                                                14; Indels
                                                                                                                                                                                                                         Query Match
93.9%; Score 2176.5; DE
Best Local Similarity 94.8%; Pred. No. 6e-195;
Matches 402; Conservative 5; Mismatches 1
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Patent No. 6734288
GENERAL INFORMATION:
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Filvaroff, Ellen
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Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
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APPLICANT: Botstein, David
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Goddard, Audrey
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                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-32
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US-09-944-457-32
                                                                                                         SEQ ID NO 32
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GENERAL INFORMATION:
APPLICANT: Masiakowski, Piotr
TITLE OF INVENTION:
FILE OF INVENTION: No. 6207413e1 Orphan Receptors
FILE OF PINTENTION: No. 6207413e1 Orphan Receptors
FILE REFERENCE: REG 630
CURRENT APPLICATION NUMBER: US/09/120,601
GURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: 09/012,072
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 405
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Best Local Similarity 100.0%; Pred. No. 5.1e-198;
Matches 405; Conservative 0; Mismatches 0;
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US-09-866-028-32
; Sequence 32, Application US/09866028
; Patent No. 6642560
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Grimaldi, Christopher
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Gerritsen, Mary
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APPLICANT: Botstein, David
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Tumas, Daniel
Wood, William
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CREARLY FILING DATE: 2001-05-26
PRIOR PELICATION NUMBER: 00/066.28
PRIOR FILING DATE: 2001-05-26
PRIOR FILING DATE: 1001-05-26
PRIOR FILING DATE: DOCU-05-26
PRIOR PELICATION NUMBER: 60/069.334
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: DECEMBER 11, 1997
PRIOR PELING DATE: DECEMBER 11, 1997
PRIOR PELING DATE: DECEMBER 11, 1997
PRIOR PELING DATE: DECEMBER 11, 1997
PRIOR PELING DATE: DECEMBER 16, 1997
PRIOR PELING DATE: DECEMBER 17, 1997
PRIOR PELING DATE: PELEBRARY 60/070, 408
PRIOR PELING DATE: PELEBRARY 60/070, 408
PRIOR PELING DATE: PELEBRARY 60/070, 408
PRIOR PELING DATE: PELEBRARY 60/070, 408
PRIOR PELING DATE: PELEBRARY 60/112, 256
PRIOR PELING DATE: PELEBRARY 60/112, 256
PRIOR PELING DATE: PELEBRARY 60/112, 256
PRIOR PELING DATE: PELEBRARY 60/112, 256
PRIOR PELING DATE: PELEBRARY 60/112, 256
PRIOR PELING DATE: DECEMBER 27, 1998
PRIOR PELING DATE: DECEMBER 17, 1999
PRIOR PELING DATE: PELEBRARY 60/112, 256
PRIOR PELING DATE: DECEMBER 17, 1999
PRIOR PELING DATE: PELEBRARY 60/112, 256
PRIOR PELING DATE: DECEMBER 17, 1999
PRIOR PELING DATE: PELEBRARY 60/112, 259
PRIOR PELING DATE: PELEBRARY 60/112, 259
PRIOR PELING DATE: PELBRARY 60/112, 251
PRIOR PELING DATE: PELBRARY 60/112, 251
PRIOR PELING DATE: PELBRARY 60/112, 2009
PRIOR APPLICATION NUMBER: PCT/USS9/2801
PRIOR PELING DATE: PELBRARY 60/112, 2009
PRIOR PELING DATE: PELBRARY 60/112, 2009
PRIOR PELING DATE: PELBRARY 60/112, 2009
PRIOR PELING DATE: PELBRA
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240 180 297 120 177 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 300 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSFWSHPTAASTPRSERPGPGGGVCEPRGGE 360 357 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGAA 420 57 118 ARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP 238 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACLDS ENCODING THE SAME FILE REFERENCE: P2548P1C1 1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW Gaps 3; Length 422; 14; Indels Score 2176.5; DB 2; Pred. No. 6e-195; 5; Mismatches 14; CURRENT APPLICATION NUMBER: US/09/945,584 PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 32
LENGTH: 422 ce 32, Application US/09945584 No. 6908993 Gerritsen, Mary Goddard, Audrey Godowski, Paul Grimaldi, Christopher 93.9%; nilarity 94.8%; Conservative Filvaroff, Ellen Gurney, Austin Hillan, Kenneth Kljavin, Ivar Napier, Mary APPLICANT: Baker, Kevin APPLICANT: Botstein, David Roy, Margaret Tumas, Daniel ; ORGANISM: Homo Sapien US-09-944-457-32 Eaton, Dan Similarity RGPA 424 RGPA 421 GENERAL INFORMATION: RESULT 7 US-09-945-584-32 402; ; Sequence 32, ; Patent No. 69 361 358 APPLICANT:
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APPLICANT: Query Match Best Local S Matches 402 298 421 418 241 301 61 121 APPLICANT: APPLICANT: TYPE: PRT APPLICANT: APPLICANT APPLICANT 셤 셤 ਨੇ 셤 ઠે d ઠે 셤 ò 셤 Š ઠ 셤 ð ଚ

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PRIOR PELLING DATE: 2001-09-26
PRIOR PELLONTON NUMBER: 09(866,028
PRIOR PELLING DATE: 2001-06-25
PRIOR PELLONTON NUMBER: 60/065,131
PRIOR PELLING DATE: BOG-666,331
PRIOR PELLONTON NUMBER: 60/065,131
PRIOR PELLONTON NUMBER: 60/065,131
PRIOR PELLONTON NUMBER: 60/065,132
PRIOR PELLONTON NUMBER: 60/065,132
PRIOR PELLONTON NUMBER: 60/065,132
PRIOR PELLONTON NUMBER: 60/065,636
PRIOR PELLONTON NUMBER: 60/065,636
PRIOR PELLONTON NUMBER: 60/065,636
PRIOR PELLONTON NUMBER: 60/065,637
PRIOR PELLONTON NUMBER: 60/065,637
PRIOR PELLONTON NUMBER: 60/065,637
PRIOR PELLONTON NUMBER: 60/065,937
PRIOR PELLON PER December 15,199
PRIOR APPLICATION NUMBER: 60/065,937
PRIOR PELLON PELLON NUMBER: 60/070,440
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58 ATCSVHGDPPGATAEGLYWTLNGRRLPPBLSRVLNASTLALALANINGSRQRSGDNLVCH 117
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APPLICANT: Napler, Mary
APPLICANT: ROY, Margaret
APPLICANT: The SAME
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P2548PIC1
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                                                                                                                                                                                                                 93.9%; Score 2176.5; DE
94.8%; Pred. No. 6e-195;
tive 5; Mismatches 1
PRIOR APPLICATION NUMBER: PCT/USO0/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 32
LENGTH: 422
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Patent No. 6929947
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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Filvaroff, Ellen
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Best Local Similarity 94.8
Matches 402; Conservative
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
                                                                                                                                      TYPE: PRT
CORGANISM: Homo Sapien
US-09-945-584-32
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US-09-944-944-32
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CURRENT APPLICATION NUMBER: US/09/944,944

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PRIOR APPLICATION UNMERS: 00/06/05/134
PRIOR APPLICATION UNMERS: 00/06/05/134
PRIOR APPLICATION UNMERS: 00/06/05/134
PRIOR APPLICATION UNMERS: 00/06/05/134
PRIOR APPLICATION UNMERS: 00/06/05/134
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION UNMERS: 00/06/05/136
PRIOR APPLICATION UNMERS: 00/06/05/126
PRIOR APPLICATION UNMERS: 00/06/05/126
PRIOR APPLICATION UNMERS: 00/06/05/126
PRIOR APPLICATION UNMERS: 00/06/05/126
PRIOR PILING DATE: December 12, 1997
PRIOR PILING DATE: December 16, 1996
PRIOR PILING DATE: December 16, 1996
PRIOR PILING DATE: December 16, 1996
PRIOR PILING DATE: December 16, 1996
PRIOR PILING DATE: December 16, 1996
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PRIOR PILING DATE: December 16, 1996
PRIOR PILING DATE: December 16, 1996
PRIOR PILING DATE: December 16, 1996
PRIOR PILING DATE: December 16, 1999
PRIOR APPLICATION UNMERS: 60/1029/28409
PRIOR PILING DATE: December 16, 1999
PRIOR APPLICATION UNMERS: PCT/US99/23019
PRIOR APPLICATION UNMERS: PCT/US99/23019
PRIOR PILING DATE: PEDELUAY 1, 1999
PRIOR PILING DATE: PEDELUAY 1, 2099
PRIOR PILING DATE: PEDELUAY 1, 2090
PRIOR PILING DATE: PEDELUAY 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PIC1
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                          93.9%; Score 2176.5; DB 2; Length 422; 94.8%; Pred. No. 6e-195; ive 5; Mismatches 14; Indels 3;
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PRIOR APPLICATION NUMBER: PCT/USO0/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 32
LENGTH: 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32, Application US/09945587 Patent No. 6936254 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
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Filvaroff, Ellen
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Best Local Similarity 94.8
Matches 402; Conservative
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APPLICANT: Botstein, David
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Napier, Mary
                                                                                                              TYPE: PRT
ORGANISM: Homo Sapien
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US-09-945-587-32
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APPLICANT:
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APPLICANT:
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APPLICANT:
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PRIOR PELICATION NUMBER: 00/165,26

PRIOR PELICATION WUMBER: 00/165,26

PRIOR FILING DATE: 20010-65-26

PRIOR FILING DATE: 10010-65-26

PRIOR FILING DATE: 10010-65-26

PRIOR FILING DATE: 10010-65-26

PRIOR FILING DATE: 100-66-30

PRIOR FILING DATE: 100-66-30

PRIOR FILING DATE: 100-69-30

PRIOR PELICATION WUMBER: 60/169,125

PRIOR PELICATION WUMBER: 60/169,125

PRIOR PELICATION WUMBER: 60/169,125

PRIOR PELING DATE: December 11, 1997

PRIOR PELING DATE: December 11, 1997

PRIOR PELING DATE: December 16, 1997

PRIOR PELING DATE: December 16, 1997

PRIOR PELING DATE: December 17, 1998

PRIOR PELING DATE: December 17, 1998

PRIOR PELING DATE: December 17, 1998

PRIOR PELING DATE: DECEMBER: 60/100,440

PRIOR PELING DATE: DECEMBER: 60/100,440

PRIOR PELING DATE: PERINARY 5, 1998

PRIOR PELING DATE: DECEMBER: 60/100,440

PRIOR PELING DATE: DECEMBER: 60/100,941

PRIOR PELING DATE: PERING DATE: DECEMBER: 60/100,941

PRIOR PELING DATE: PERING DATE: DECEMBER: 60/100,941

PRIOR PELING DATE: DECEMBER: 60/100,941

PRIOR PELING DATE: PERING DA
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                                                                                                                                                                                                                             DB 2; Length 422;
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                                                                                                                                                                                                                         93.9%; Score 2176.5; DB
94.8%; Pred. No. 6e-195;
tive 5; Mismatches 1
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 32
LENGTH: 422
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APPLICANT: Lok, Si
APPLICANT: Lok, Si
APPLICANT: Glamberg, Anna C.
APPLICANT: Glamberg, Anna C.
APPLICANT: Glamberg, Anna C.
APPLICANT: Glamberg, Anna C.
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Lehner, Joyce M.
TITILE OF INVENTION: MAMMALIAN ZC.
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: Zymogenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
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Patent No. 6271343
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.8
Matches 402; Conservative
                                                                                                                                        TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-32
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US-09-071-224-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
93.8%; Score 2172.5; DB 2; Length 422;
Best Local Similarity 94.6%; Pred. No. 1.4e-194;
Matches 401; Conservative 6; Mismatches 14; Indels 3;
FastSEQ for Windows Version 2.0
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
                                                                     CLASSIPCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELEPHONE: 206-442-6678
TELEPHONE: 206-442-6678
                                                                                                                                                                                                                                                                                                                                           LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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                                                             PILING DATE
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Sequence 19, Application US/09071224
; Patent No. 6271343
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Presnell, Scott R.
APPLICANT: Usinberg, Anna C.
APPLICANT: Glibert, Teresa
APPLICANT: Glibert, Teresa
APPLICANT: Foster, Donald C.

US-09-071-224-19

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101 LALANINGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTP 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 GAHGETFLHTNYSLKYKLRWYGQDNTCBEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL 220
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Pred. No. 1.4e-187;
0; Mismatches 1;
                                                                                                                                                                             COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHKTRNQDEGILPSGRRGAARGPAG 385
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFRENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INPORMATION:
TELEPHONE: 206-442-6627
                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 19
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Best Local Similarity 99.7%;
Matches 384; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 385 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-224-19
                                                                                                                                                              ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                               STATE: WA
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                  USA
                                                                                                                                                 COUNTRY:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
                   Sequence 12, Application US/09521335
Fatent No. 6800460
GENERAL INFORMATION:
APPLICANT: Oppmann J Birgit
APPLICANT: Timans, Jacqueline C.
APPLICANT: Timans, Jacqueline C.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
TITLE REFERENCE: DX0935K
CURRENT PILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE PATENTIN VOIC: 2.0
SEQ ID NO 12
LENGTH: 410
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
90.4%; Score 2095; DB 2; Length 410;
Best Local Similarity 93.9%; Pred. No. 2.4e-187;
Matches 388; Conservative 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lok, Si
APPLICANT: Presnell, Scott R.
APPLICANT: Jeluberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Goster, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Zymogenetics
1201 Eastlake Ave East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09071224 Patent No. 6271343 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               ; ORGANISM: primate US-09-521-335-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seattle
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STREET: 120
               -09-521-335-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-071-224-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 ARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLICRWTPGAHGETFLHTNYSLKYKLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 90.4%; Score 2094; DB 2; Best Local Similarity 94.8%; Pred. No. 3.1e-187; Matches 386; Conservative 5; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09120601
Patent No. 6207413
GENERAL INFORMATION:
APPLICANT: Masiakowski, Piotr
TITLE OF INVENTION: No. 6207413el Orphan Receptors
FILE REFERENCE: REG 630
                                                                SOFTWARE: FastSEQ for Windows Version 2.0 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/071,224 FILING DATE: CLASSIFICATION: PRIOP ADDR.
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LAUN, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-2:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
COMPUTE: JOACE COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPETIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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                                                                                                                                                                                                                                                                  Length 448;
                                                                                                                                                                                                                                                                                                          13; Indels
                                                                                                                                                                                                                                                                Query Match 89.4%; Score 2071.5; DB 2; Best Local Similarity 90.0%; Pred. No. 4.3e-185; Matches 386; Conservative 5; Mismatches 13;
CURRENT APPLICATION NUMBER: US/09/120,601
CURRENT FILING DATE: 1998-07-22
BARLIER APPLICATION NUMBER: 09/012,072
BARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6
LENGTH: 448
TYPE: PRT
TYPE: PRT
ORGANISM: HUMAN
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Patent No. 6271343
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Defence, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MANWALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Zymogenetics
STREET: 1201 Eabtlake Ave East
CITY: Seattle
STATE: WA
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ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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US-09-071-224-17
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241 RYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPT 300
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Pred. No. 2.9e-183;
6; Mismatches 8;
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: LAUN, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECHMUNICATION INFORMATION:
TELEPHONE: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 MOKSHKTRNODEGILPSGRRGTARGPA 387
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SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 96.4
Matches 373; Conservative
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April 11, 2006, 02:03:38; Search time 115.031 Seconds (without alignments) 1608.075 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
geneseqp2003bs:*
geneseqp20048:*
geneseqp2005s:*
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DB seq length: 200000000
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2290
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                                                                                                                                                                                 Title:
Perfect score:
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Maximum I
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AABOO826 Wirine ha	Aav05782 Himan	Aav06479 Human	Human	9 Aay26339 Human	Aab01316 Human	3686 Amino aci	3545 Amino aci		Abu60235 Human	Abg72776 Human	Abu64921 Human	8355 Abu58355 Novel hum	Abu57241 Human	6306 Abu56306 Human sec	Abu60346	1307 Abul1307 Human pro	Abu67126 Human	5788 Adc25788 Human sec	ADC25546 Human sec	5667 Adc25667 Human sec	Adh27452	1501 Ade71501 Human sec	
) A	AAEO	AAYO	AAYO	AAY1	AAY2633	AAB01316	AAY93686	AAG6354	ABU55925	ABU60235	ABG72776	ABU64921	ABU58355	ABU57241	ABU56306	ABU60346	ABU11307	ABU67126	ADC25788	ADC2	ADC25667	ADH27452	ADE71501	
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o Y	02-JUL-2001	(first	t entry)	ŝ			
	Murine haemopoietin	nopoieti		pto	receptor, NR6 protein, encoded by NR6 1	DNA.	
Σ Ο τ <u>8</u> <u>8</u> 8	urine; bic ardiotropl	logical lin-like	ly act	ive	Murine; biologically active complex; haemopoletin receptor; NR6; cardiotrophin-like cytokine; CC; therapy; prophylaxis; prolifer differentiation of a marginal marginal and ma	or; NR6; proliferation;	
	TITELETICI	, increase	10 110	1	var, meanotrophic activity.		
SOS	Mus sp. Unidentified	ģ.					
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Fabri LJ, Reid K, Bartlett PF, Hilton DJ; (AMRA-) AMRAD OPERATIONS PTY LTD. 08-OCT-1999; 99AU-00003327. 12-MAY-2000; 2000AU-00007489. 06-OCT-2000; 2000WO-AU001216. WO200127157-A1. 19-APR-2001.

Nash A, Jachno KM, F Nakata Y, Hasegawa M; WPI; 2001-281978/29. N-PSDB; AAD04199.

Claim 29; Page 106-107; 123pp; English.

New biologically active complex comprising NR6 and cardiotrophin-like-cytokine, for facilitating proliferation, differentiation and/or survival of a cell.

The present invention relates to a biologically active complex comprising a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC). The complex is useful in the manufacture of a medicament for the treatment and/or prophylaxis of a subject, as it is involved in facilitating proliferation, differentiation and/or survival of a cell. The complex or its components have neurotrophic activity. The present sequence is murine

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Local Similarity
                                                              N-PSDB; AAX25489
                                                                                                                                                                                                                                                                                             Sequence 422 AA;
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                                                                                                                                        61 VHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANINGSRQRSGDNLVCHARDG
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                                                                                         1 MPAGRRGPAAQSARRPPPLLPLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCS
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                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GBRI-ILR; hGBR-ILR; cytokine receptor; human; cancer; obesity; inflammation; septic shock; AIDS; embryo development; lung infection cytostatic; anorectic; immunosuppressive; antibacterial; antiviral; antiinflammatory; therapy.
                   Revised record issued on 09-SEP-2004 : Correction to Organism field
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                                                     Length 421;
                                                                       Indels
haemopoietin receptor, NR6 protein, encoded by NR6 DNA
                                                     100.0%; Score 2290; DB 4;
100.0%; Pred. No. 5.1e-185;
ive 0; Mismatches 0;
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                                                                        Matches 421; Conservative
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38. .42
                                                     Query Match
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The present sequence represents a novel type 1 cytokine receptor that has been termed human GBRI-ILR as it is believed to be an interleukin creceptor, or at least a substantial part of such a receptor. The sequence is predicted from an isolated full-length cDNA clone (see AAX25489) cobtained from a human placental CDNA library. GBRI-ILR mRNA is expressed cost strongly in spleen, thymus, lymph node, appendix, bone marrow, thyroid, adrenal cortex, stomach, heart, placenta and skeletal muscle, suggesting a role for GBRI-ILR in the immune system. In human foctal tissue, strong expression is seen in the lung, but not in brain, kidney cor liver. A GBRI-ILR receptor has also been identified in mice (see AAX05783). The high degree of conservation of amino acids between the human and murine polypeptides indicates that this receptor is concists and antagonists can be used to treat e.g. cancer, immune caponists and antagonists can be used to treat e.g. cancer, immune caponists can be used to treat e.g. cancer, immune capitally inview of homology to the leptin receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACBPRGGEPSS
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                                                                                                                                                                                                                                                                    Novel human or mouse type I cytokine receptors hGBRI-ILR or mGBRI-ILR, useful for treating e.g. cancer, immune disorders, obesity and AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPAGRRGPAAQSARRPPPLLP-LILLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
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Pred. No. 3.9e-184;
0; Mismatches 0;
                                                                                                                     Kosco-Vilbois M;
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99.8%;
97GB-00021961
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                                                            (GLAX ) GLAXO GROUP LTD
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359

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419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes nucleic acids encoding PRO secreted and
                                                         241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                            VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                                                                                                    LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                                                          LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                                                                                                          GPVRRELKOFLGWLKKHAYCSNLSFRLYDQWRAWMOKSHKTRNQDEGILPSGRRGTARGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, PRO protein, tumour necrosis factor family, TNF; cytokine, secreted protein; transmembrane protein; inflammation disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding PRO secreted and transmembrane proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY17825 standard; protein; 422 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Fig 17; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO327 protein sequence.
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97US-0069278P.
97US-0069334P.
97US-0069335P.
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97US-0069694P.
97US-0069696P.
97US-0069702P.
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16-DEC-1997;
16-DEC-1997;
16-DEC-1997;
17-DEC-1997;
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11-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVRATNRLGSARSDVLTLDILDVVTTDPPPD 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents human PRO327 (UNQ288), a 46.3 kDa protein (pI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MPAGRRGPAAQSARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawrence DA,
                                                                                                                                                                                PRO327; UNQ288; cancer; tumour; diagnosis; therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillan KJ,
                                                                                                                                       Human tumour-associated protein PRO327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 6; 162pp; English.
standard; protein; 422
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98US-0083500P.
98US-0086414P.
98US-0088742P.
98US-0107783P.
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                                                                                        (first entry)
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Best Local Similarity 99.8
Matches 421; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis and treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
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29-APR-1998;
22-MAY-1998;
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10-NOV-1998;
20-NOV-1998;
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PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO15; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human.
                                                                                      The present sequence is a human U4 protein which is a member of haematopoietin receptor superfamily. The protein is predicted to have following biological activities: cytokine, cell proliferation/differentiation, immune stimulating or suppressing and haematopoiesis regulating. The U4 protein can be used to treat immune disorders and deficiencies, autoimmune disorders, allergies, cancer, myeloid or lymphoid cell deficiencies and platelet disorders
                                                                                                                                                                                                                                                                                                                                                         121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYCQ
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     Novel polypeptides and polymucleotides used for treatment of human diseases and disorders e.g. immune disorders or deficiencies caused fungal, parasitic or viral infections.
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                                                                                                                                                                                                                              Length 422;
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                                                                                                                                                                                                                          Score 2279.5; DB 2;
Pred. No. 3.9e-184;
0; Mismatches 0;
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                                                   Score 2279.5; DB 2
Pred. No. 3.9e-184;
0; Mismatches 0;
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larity 99.8%;
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N-PSDB; AAX90754.
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New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
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                                                                                                                                                                               Score 2279.5; DB 3; Length 422; Pred. No. 3.9e-184; 0; Mismatches 0; Indels 1;
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/note= "N-myristoylation site"
37. .43
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/note= "signal
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A, Godowski PJ, Grimaldi CJ, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
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ce= "N-myristoylation site"
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note= "N-myristoylation site"
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04. .108
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                          note= "Amidation site"
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9. .83
note= "Amidation site"
12. .96
/label= Signal peptide
                                                                                          44. .61
|Tabel= Transmembrane
|3. .79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphorylation site"
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98US-0112850P.
98US-0113296P.
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/note= "cA
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/label= Gr
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/note= "N-
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designated as PRO
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Sequence 422 AA;
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218. .224
/note= "N-myristoylation site"
292. .296
/note= "N-glycosylation site"
300. .306
/note= "N-myristoylation site"
       4. .48
note= "casein kinase II phosphorylation site"
                                                                                                                                                          "casein kinase II phosphorylation site"
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note= "N-myristoylation site"
120. 326
'note= "N-myristoylation site"
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Note= "N-myristoylation site"
155. .361
Note= "N-myristoylation site"
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                              gite"
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"N-myristoylation site"
                                                                            note= "N-glycosylation site"
121. .127
note= "N-myristoylation site"
440. .144
note= "N-glycosylation site"
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Anote= "N-glycosylation site"

179. 185

Anote= "N-myristoylation site"
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99WO-US012125.
99WO-US020111.
99WO-US028313.
99WO-US028409.
99WO-US028301.
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/note= "N-
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104. .108
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08-MAR-1999;
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15-SEP-1999
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01-DEC-1999
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N-PSDB; AAA46902

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The present sequence represents a novel human polypeptide. The specification describes novel polypeptides designated PRO21, PRO222, PRO327, PRO1265, PRO344, PRO344, PRO347, PRO345, PRO585, PRO345, PRO585, PRO585, PRO585, The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and proliferation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuro-muscular function; tumour; instruction; ustructions system; reproductive system; tumour; immune system; haematopoletic system; reproductive system; liver; skeletal muscle; neurodegenerative disease; amyotrophic lateral sclerosis; Parkinson's disease; Huntingdon's disease; muscular mass; paralysis; cancer; obesity; fertility; endometriosis; blastocyst implantation; thrombosis; retinal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGF 420
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New anti-polypeptide antibody useful in the treatment and diagnosis of neoplastic cell growth and proliferation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 422;
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Pred. No. 3.9e-184;
0; Mismatches 0;
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                                                                             61; Fig 6; 220pp; English.
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Best Local Similarity
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New isolated PRO polypeptide and encoding nucleic acid, useful for the diagnosis and treatment of disorders associated with the PRO polypeptide, such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.
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    LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                           361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                                                                                GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PRO; secreted protein; transmembrane protein; anti-HIV; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; cardiant; AIDS; acquired immunodeficiency syndrome; cancer; atherosclerosis; inflammatory disease; diabetic complication; cardiac injury; organ failure.
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PJ, Grimaldi JC, Gurne
Roy MA, Tumas D, Wood
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99WO-US028301.
99WO-US030095.
2000WO-US003565.
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2000WO-US005841.

2000WO-US008439.

2000WO-US014042.

2000WO-US024010.

2000WO-US032678.
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99WO-US028313
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Gerritsen ME, Goαααια ...
Gerritsen II, Kljavin IJ,
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N-PSDB; ABX75462.
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01-DEC-1999;
16-DEC-1999;
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02-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human CLF-1 protein. The specification describes a complex comprising a NNT-1 protein and a CLF-1 and/or sCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate activity of the sCNTFRalpha/gpi30/LirRbeta receptor complex, or to induce chosphory/lation of the tyrosine of gpi30 and LiFRbeta, particularly where cells expressing the receptor complex are in the central or peripheral nervous system, in neurons implicated in neuro-muscular function or in skeletal muscle. The complex or antibodies are also used to decrease the survival, growth or proliferation of tumour cells or to facilitate the proliferation and/or inhibit differentiation of cells stocks. The complex is also used to modulate activity of the gpi30/LiFRbeta receptor or cells expressing that receptor, particularly those cells implicated in the immune, haematopoietic, nervous or reproductive system, the liver or skeletal muscle. Molecules of the invention may be used to prevent or treat neurodegenerative diseases including amyotrophic lateral sclerosis, muscular tissue or to maintain muscular mass in paralysis patients. They
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             may also be used to treat cancer, obesity and associated diseases, and to improve fertility, particularly to avoid endometriosis and/or assist blastocyst implantation, thrombosis, or retinal disease, particular
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                                                                                                                                                                                                                                                                                                                                                                                      A complex comprising a NWT-1 protein and a CLF-1 and/or sCNTFRalpha protein useful to treat neurodegenerative disease including Parkinson's
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                                                                                                                                                                                                                                                                                      Gascan H;
                                                                                                                                                                                                                                                                                  Plun-Favreau H, Chevalier S,
                                                                                                                                                                                                                                         (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                              and Huntington's, obesity and cancer.
                                                                                                                                                                                                                      (FABR ) FABRE MEDICAMENT SA PIERRE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 63-64; 67pp; French.
                                                                                                                    26-JAN-2001; 2001WO-FR000253.
                                                                                                                                                                                2000FR-00013089.
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Matches 421; Conservative
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                                      WO200155172-A2.
Homo sapiens
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positives when compare to with its associated signal petitie; or (b) at least 80% sequence identity to a sequence encoded by the full-length coding sequence of a DNA deposited in the American Type Culture Collection (ATCC). Also included are: (1) an isolated nucleic acid comprising: (a) at least 80% sequence identity to a nucleotide sequence controlled are: (1) an isolated nucleic acid comprising: (a) at least 80% sequence identity to a nucleotide sequence or full-length coding sequence identity to a nucleotide sequence or full-length coding sequence with any of 15 fully defined sequence or full-length coding sequence of a full-length coding sequence of a controlled are a RNO protein; (b) at least 80% sequence of a full-length coding sequence of a controlled are after a full-length coding sequence of a controlled are are a full-length coding sequence of a controlled are a full-length coding sequence of a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a controlled are a contro
positives when compared to any of 15 sequences, fully defined in the
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Sequence 422 AA;

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                                   Gaps
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 6; Length 422;
                                   0; Indels
99.5%; Score 2279.5; DB 6
99.8%; Pred. No. 3.9e-184;
ive 0; Mismatches 0;
               Best Local Similarity 99.8 Matches 421; Conservative
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ABU60235 standard; protein; 422 AA.

RESULT

(first entry)

24-APR-2003

ABU60235;

Human PRO polypeptide #6.

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Human; PRO; secreted polypeptide; transmembrane polypeptide; cancer; inflammatory disease, atherosclerosis; cardiac injury; AIDS; infertility; birth defect; premature aging; diabetes; dog; cat; horse; acquired immunodeficiency syndrome; cow; sheep; pig; goat; rabbit; industry; cytostatic; antiinflammatory; cardiant; antiinfertility; anti-HIV; antiarteriosclerotic; antidiabetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New secreted and transmembrane polypeptides (e.g. PRO241, for use in pharmaceuticals, diagnostics or bioreactors, particularly for detecting or treating e.g. cancers, infertility or acquired immunodeficiency syndrome in mammals.
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970S-0069334P-
970S-0069425P-
970S-0069694P-
970S-00696702P-
970S-0069870P-
970S-0069873P-
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02-MAR-2000;
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bioreactors. These are particularly useful for detecting or treating cancers, inflammatory diseases, atherosclerosis, cardiac injury, inflammatory diseases, atherosclerosis, cardiac injury, inflammatory defects, premature aging, acquired immunodeficiency syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are also useful in biotechnological and medical research and in various industrial applications. Sequences ABU60230-ABU60245 represent human PRO
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                                                                                                                                                                                                                     Score 2279.5; DB 6
Pred. No. 3.9e-184;
0; Mismatches 0;
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                                                                                                                                          polypeptides of the invention
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Best Local Similarity
                                                                                                                                                                                  Sequence 422 AA;
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The invertion discusses a merical to the comparing time during bone to cartilage formation. The method comprises determining levels of RNA from the genes to obtain levels of expression and comparing these to a set of reference levels for each of the genes. Bone formation is an est of reference levels for each of the genes. Bone formation is an estential process in embryonic development and plays a critical role in essential process and conditions in humans. Two genes found to be regulated during bone and cartilage formation are the cytchine receptor-like factor (during bone and cartilage formation are the cytchine receptor-like factor cell differentiation, and matrix metalloproteinase 23 (MMP23), which is specifically regulated during mesenchymal computer program for analysing levels of expression of a number of genes, compositions comprising a number of antagonists or agonists of the genes and methods for determining whether a subject has, or is likely to develop, a disease related to bone or cartilage formation or resorption, for identifying a compound for treating, modulating or stimulating a disease related to bone or cartilage formation possibly acting as a cadherin or CD8 agonist or a cytokine antagonist. The methods and compositions are useful for cartilage formation such as osteodystrophy, osteohypertrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteolytic lesions produced by bone metastasis, bone loss due to mimobilisation or sex hormone deficitiency, bone and cartilage loss caused by an inflammatory disease, rheumatoria arthritis, osteoarthritis and bone fractures. The sequence presented is the human CLP-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention discloses a method for determining the difference between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANINGSRQRSGDNLVCHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                             Determining the difference between levels of expression of a number genes, useful for diagnosing and treating disorders associated with or cartilage formation or resorption such as osteoporosis and bone
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Pred. No. 3.9e-184;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 192-193; 197pp; English
                                                              18-APR-2002; 2002WO-US012149
                                                                                                      18-APR-2001; 2001US-0284786P.
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                                                                                                                                                                                        B, Pittman
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N-PSDB; ABX14013
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                    31-0CT-2002
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LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
25-MAY-2001; 2001US-00866028.
                              (GETH ) GENENTECH INC
                                                                           2003-311003/30.
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                Sequence 422 AA;
                                                                                   N-PSDB; ABX96790
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                                                                                                                                                                                                           Human, PRO; secreted protein; transmembrane protein;
cornella de Lange syndrome; gene therapy; immune disorder;
inflammatory disease; organ failure; atheroselerosis; cardiac injury;
infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
          VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                       LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                             GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                                                                                                                                                                                             Human secreted/transmembrane protein PRO327
                                                                                                                                               ABU64921 standard; protein; 422 AA
                                                                                                                                                                                                                                                                                                                 97US-0069234P.
97US-00693334P.
97US-00693335P.
97US-0069425P.
97US-0069694P.
97US-0069694P.
97US-0069873P.
97US-0079873P.
97US-0074086P.
97US-0074086P.
97US-0074086P.
97US-0074082F.
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99WO-US028313
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                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                           diabetic complication.
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                                                                                           AR 421
                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                    31-AUG-2001;
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17-DEC-1997;
18-DEC-1997;
05-JAN-1998;
09-FEB-1998;
25-FEB-1998;
16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-1999;
28-JUL-1999;
15-SEP-1999;
30-NOV-1999;
                                                                                                                                                                              15-MAY-2003
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16-DEC-1999
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The invention relates to an isolated nucleic acid encoding a secreted/
transmembrane polypeptide (designated as PRO proteins). 15 PRO
Cransmembrane polypeptide (designated as PRO proteins). 15 PRO
Critical and their encoding polymucleotides are disclosed. Also
included are a vector comprising the PRO nucleic acid, a host cell
comprising the vector, a process for producing a PRO polypeptide (by
conjugation and recovering the PRO polypeptide from the expression of the PRO
polypeptide, and recovering the PRO polypeptide from the cell culture, an
cisolated polypeptides a chimaeric molecule comprising PRO fused to a
heterologus annio acid sequence and an antibody which specifically binds
to PRO. The PRO nucleotide sequences are useful as hybridisation probes,
in chromosome and gene mapping, in generating sense and antisense RNA or
CC PNA, in generating transgenic or knock-out animals which can be used in
ct he development and screening of therapeutically useful reagents, and in
cc ene therapy. The polypeptides may be used as molecular weight markers
cc for protein electrophoreais purposes. The PRO polypeptides and nucleic
acids may also be used for chromosome identification, and tissue typing.
CC acids may also be used for chromosome identification, and tissue typing.
CR syndrome. Other PRO proteins are variously implicated in immune
cc syndrome. Other PRO proteins are variously implicated in immune
cc injury, infertility, birth defects, premature aging, cardiac injury,
c injury, infertility, birth defects, premature aging, cardiac injury,
considered and diabetic complications. The present sequence represents
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                                                                                                                                                                                                                                                                                                                    New transmembrane polypeptides and polymucleotides useful for chromosome identification, tissue typing, gene therapy, in chromosome and gene mapping, or as molecular weight markers.
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Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL,
Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
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99.8%; Pred. No. 3.9e-184;
iive 0; Mismatches 0;
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(GETH ) GENENTECH INC.
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                                            WPI; 2003-198285/19.
                                                    N-PSDB; ABX78444.
                                                                                                                                                                             Sequence 422 AA;
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                      Gerritsen MB,
                                                                                          complications
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                               Hillan KJ,
                Baker KP,
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                                                                                                                                            Human; antiinflammatory; antiarteriosclerotic; cardiant; gynecological;
anti-HIV; cytostatic; antidiabetic; BMP-agonist; BMP-Antagonist;
cytokine-agonist; cytokine-antagonist; gene-Therapy;
inflammatory disease; organ failure; atherosclerosis; cardiac injury;
infertility; birth defect; premature aging; AIDS; cancer;
GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
        GPVRRELKQFLGWLKKHAYCSNLSFRLYDOWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                                                                                                                              Novel human secreted protein PRO327
                                                                                 ABU58355 standard; protein; 422 AA.
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9705-0069334P
9705-0069425P
9705-0069694P
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9805-00128517
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2000WO-US008439
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2001US-00866028
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                                                                                                                 (first entry)
                                                                                                                                                                                   diabetic complication
                             421
                                            AR 422
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                                                                                                                                                                                                   Homo sapiens.
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25-MAY-2001;
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12-DEC-1997
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              361
360
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                                                                                                ABU58355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                              New isolated PRO polypeptide and encoding nucleic acids, useful for the diagnosis and treatment of disorders such as inflammatory disease, atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a novel isolated PRO polypeptide. The methods a compositions of the present invention are useful for the diagnosis and treatment of disorders such as inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications and mutations in general. This is the amino acid sequence of a novel human secreted PRO protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPAGERGPAAQSARPPPILPLILLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNTCEEYHTVGPHSCHI PKOLALFTPYE I WVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 LKPGTVYFVQVRCNPPGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPAGRRGPAAQSARRPPELLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
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   Eaton DL, Ferrara N, Filvaroff E;

), Godowski PJ, Grimaldi JC, Gurney AL;

Napier MA, Roy MA, Tumas D, Wood WI;
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Pred. No. 3.9e-184;
0; Mismatches 0;
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Botstein D, Eat
Æ, Goddard A,
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Matches 421; Conservative
                                                                 Kljavin 1J,
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SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANINGSRQRSGDNLVCHARD 120
                                                                            361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWWQKSHKTRNQDEGILPSGRRGTARGP 420
                                                      GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gynecological; anti-HIV; cytostatic; antidiabetic; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome;
                                                                                                                                                                                                                        VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                                                                                                                                     DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                   VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                                                                                                              DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
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9705-0069334P
9705-0069435P
9705-0069644P
9705-00696702P
9705-0069870P
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9805-0070492P
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9805-01132850P
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16-DEC-1997;
16-DEC-1997;
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17-DEC-1997;
18-DEC-1997;
18-DEC-1997;
05-JAN-1998;
09-FEB-1998;
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22-DEC-1998;
02-JUN-1999;
28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a nucleotide sequence encoding an isolated secreted and/or transmembrane protein. The nucleotide sequences of the invention may have antiinflammatory, antiarteriosclerotic, cardiant, anti-infertility, anti-HTV, cytostatic and antidiabetic activities and may be used in gene therapy. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a protein encoded by the nucleic acids of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or
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                  antiinflammatory; anti-HIV; antiarteriosclerotic; cardiant; infertility; anti-infertility; anti-infertility; anti-infertility; anti-infertility; anti-infertility; anti-infertility; anti-inflammatory disease; organ failure; atherosclerosis; cardiac injury; premature aging; AIDS; cancer; diabetic complication.
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     anti-infertility; anti-HIV; cytostatic; antidiabetic; transmembrane;
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A, Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
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va. Goddard A, Godowski r
TT. Napier MA,
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99WO-US028113.
99WO-US028409.
99WO-US028301.
99WO-US030095.
2000WO-US003565.
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2000WO-US020710
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30-NOV-1999;
01-DEC-1999;
16-DEC-1999;
11-FEB-2000;
22-FEB-2000;
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28-FEB-2001;
25-MAY-2001;
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30-MAR-2000;
22-MAY-2000;
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New isolated PRO polypeptide and encoding nucleic acids, useful for the diagnosis and treatment of disorders such as inflammatory disease, atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
                                                                                                                                                                                                Gurney AL;
                                                                                                                                                                                    Baker KP, Botstein D, Eaton DL, Perrara N, Filvaroff B;
Gerritsen MB, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL,
Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
                                                                                                                                                                                                                                                                                                                    Claim 12; Fig 14; 171pp; English.
                                                  11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US004414.
02-MAR-2000; 2000WO-US005841.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
28-JUL-2000; 2000WO-US0326710.
01-DEC-2000; 2000WO-US0326710.
                     99WO-US028409.
99WO-US028301.
99WO-US030095.
2000WO-US003565.
                                                                                                                              28-FEB-2001; 2001WO-US006520
25-MAY-2001; 2001US-00866028
                                                                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                              WPI; 2003-147446/14.
N-PSDB; ABX75909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 422 AA;
                                                                                                                                                                                                                                                                                               complications.
15-SEP-1999;
30-NOV-1999;
30-NOV-1999;
01-DEC-1999;
16-DEC-1999;
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The invention relates to an isolated PRO polypeptide having at least 80% amino acid sequence identity to and scoring at least 80% positives when compared to any of 15 fully defined sequences of 235-954 amino acids, given in the specification. Also included are: (1) an isolated PRO conscience to a specification of the sequence identity to a nucleotide sequence that encodes PRO or its extracellular domain, and comprising any of 15 fully defined nucleotide sequences of 957-3441 bp, given in the specification and deposited under ATCC accession number 209526, 209526, 209528, 209528, 209528, 209528, 209528, 209528, 209528, 209529, 209527, 209570, 209618, 209619; (2) a vector comprising the PRO nucleic acid; (3) a host cell comprising the vector; (4) producing PRO polypeptides, comprising culturing the cell for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture; (5) a chimaeric molecule comprising PRO polypeptide and recovering the PRO polypeptide and recovering the PRO polypeptide and recovering the pRO polypeptide and compositions are useful for the diagnosis and treatment of methods and compositions are useful for the diagnosis and treatment of disorders such as inflammatory disease, organ failure, atheroscalerosis, cardiac injury, infertility, birth defects, premature aging, AIDS (acquired immunodeficiency syndrome), cancer, diabetic complications and mutations in general. The present sequence is a a PRO polypeptide 1; 179 239 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANINGSRQRSGDNLVCHARD 119 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120 121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180 DNTCEEYHTVGPHSCHIPKDLALPTPYEIWVRATNRLGSARSDVLTLDILDVVTTDPPPD 240 23 9 1 MPAGRRGPAQSARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ DNTCEEYHTVGPHSCHIPKDLALPTPYRIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 1; Gaps DB 6; Length 422; Query Match 99.5%; Score 2279.5; DB 6; Length Best Local Similarity 99.8%; Pred. No. 3.9e-184; Matches 421; Conservative 0; Mismatches 0; Indels 9 61 120 180 181

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요 ઠે

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419 360 420 VHVSRVGGLBDQLSVRWVSPPALKDFLFQAKYQIRYRVBDSVDWKVVDDVSNQTSCRLAG 299 241 VHVSRVGGLBDQLSVRWVSPPALKDFLFQAKYQIRYRVBDSVDWKVVDDVSNQTSCRLAG 301 LKPGTVYFVQVRCNPFGIYGSXKAGIMSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACBPRGGEPSS 421 AR 422 Æ 240 360 300 361 420 421 ઠે ద ò 셤 δ 셤 ò 셤

Search completed: April 11, 2006, 02:09:57 Job time : 116.031 secs

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sw model protein search, using OM protein - Run on:

April 11, 2006, 02:10:19; Search time 21.0667 Seconds (without alignments) 1922.808 Million cell updates/sec

US-09-037-657-44 2290 Title: Perfect score:

1 MPAGRRGPAAQSARRPPPLL......NQDEGILPSGRRGTARGPAR 421 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seq seq Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	prolactin receptor	prolactin receptor		membrane glycoprot	glycoprotein 130 -	prolactin receptor	interleukin-6 sign	prolactin receptor	prolactin receptor	lactogen receptor	prolactin receptor	granulocyte colony	ciliary neurotroph	granulocyte colony	granulocyte colony ·	granulocyte colony	ciliary neurotroph	growth promoting a	interleukin-11 rec	interleukin-11 rec	interleukin-6 rece	leukemia inhibitor							
SUMMARIES																														
SUMIN		940	A59405	A40144	A36337	149699	150455	A44257	A29884	A41070	A34631	A36116	177525	177524	153269	JQ1655	145971	A30304	151086	A34898	158141	B38252	JH0329	C38252	CHHOCN	S60614	137891	148343	A41242	S17308
	DB	5	7	~	7	~	7	7	N	~	~	~	~	7	7	~	~	7	7	~	~	~	N	7	н	~	~	~	7	0
	Query Match Length	288	376	622	918	917	830	918	310	412	610	610	292	303	608	831	581	919	630	837	372	171	783	863	372	362	422	432	468	1097
d	Query Match	14.5	14.5	14.5	14.1	13.9	13.8	13.7	13.7	13.7	13.7	13.7	13.5	13.5	13.5	13.4	13.4	13.1	11.5	11.2	10.9	10.6	10.6	10.6	10.3	9.5	9.5	9.1	8.8	8.7
	Score	332	332	332	323	317.5	316	314.5	313	313	313	313	309.5	309.5	309.5	308	306.5	300.5	263.5	255.5	249	242.5	242.5	242.5	236	211.5	211.5	208.5	201	200
	Result No.		7	m	4	7	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

interleukin-6 rece	prolactin receptor	leptin receptor, s	leptin receptor, s	leptin receptor, s	leptin receptor, s	leptin receptor, s	hematopoietic grow	interleukin-6 rece	lactogen receptor	leptin receptor, 0	proto-oncogene - m	differentiation-st	MPL-K protein prec	MPL-P protein prec	leptin receptor, i
JL0145	A32868	S68441	S68439	S68437	S68440	S68438	835317	JL0144	B34631	PC4184	837622	JX0312	B45266	A45266	874225
~	~	~	N	N	N	N	~	~	N	Ŋ	N	~	~	~	~
460	156	805	892	894	900	1162	625	440	150	1162	626	1092	579	635	895
8.7	8.7	8.5	8.5	8.5	8.5	8.5	8.5	8.4	8.3	8.3	8.3	8.2	8.1	8.1	8.0
199.5	199	194.5	194.5	194.5	194.5	194.5	194	191.5	191	190.5	190	187	186.5	186.5	184
30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

prolactin receptor short form S1b precursor, breast cancer cells T-47D - human C;Species: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: B59405; B49400
R;Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A;Rition and characterization of two novel forms of the human prolactin recep. A;Reference number: A59405; MUID:21538812; PMID:11518703

A;Status: preliminary

A,Molecule type: DNA A,Residues: 1-288 <HU1> A,CRSS-references: UNIPROT:Q96P36; UNIPARC:UPI00006CDDA; GB:AF214012; PIDN:AF214012.1 R;Hu, Z.Z.

submitted to GenBank, Decer A, Reference number: A49400 A, Accession: B49400

A;Status: preliminary
A;Molecule type: DNA
A;Redidues: 1-288 <HUZ>
A;Cross-treferences: UNIPARC:UP1000006CDDA; GB:AF214012; PIDN:AF214012.1
C;Comment: This is one of the short forms (Sla and Slb) of the human proactin receptor ta-camein gene promoter activation, with Slb more effective than Sla. However, their live;G;Genetics:

A;Cross-references: GDB:120315; OMIM:176761
A;Map position: 5p13.3-5p13.1
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein; transmembrane protein
F;1-2-4,Domain: signal sequence #status predicted <SIG>F;2-28/Product: prolactin receptor, short form S1b #status predicted <MAT>F;36-221/Domain: cytokine receptor homology <CRS>F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Gaps 18; 14.5%; Score 332; DB 2; Length 288; 37.1%; Pred. No. 1.7e-18; tive 28; Mismatches 95; Indel8 83; Conservative Query Match Best Local Similarity Matches

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122 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 180 72 ò 셤

181 NTCERYHTVGPHSCHIPKO-LALFIPYBIWVEATWRLGSARSDVLTLDILDVVTTDPPPD

Š g

240 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 294 ઠે 셤

295 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 338

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Ajcross-references: UNIPROT:P16471; UNIPARC:UP10000132234; GB:M31661; NID:g190361; PIDN: R, Puh, G.; Wells, J.A.
J. Biol. Chem. 270, 13133-13137, 1995
A,Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li A,Reference number: A57018; MUID:95286597; PMID:7768908
A,Accession: A57018
A,Accession: A57018
A,Accession: A57018
A,Accession: A57018
A,Residues: 25-228,'AW' ARS>
A,Coross-references: UNIPARC:UP1000006D208; GB:S78505; NID:g999114; PIDN:AAB34470.1; PID: C,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane glycoprotein gp130 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 ISPESPVVQLHSNPTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
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R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an IL-6 signal transducer, A;Reference number: A36337, MUID:91084844; PMID:2261637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted
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4.4e-18;
. ~ 95; Indels ?
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28.2%; Pred. No. 3.6e-17;
ive 52; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 FKILSLHPGQKYLVQVRCKP-----DHGYWSAWSPATFIQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 5p13.3-5p13.1
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-622/Product: prolactin receptor, long form #status p
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent)
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A,Gene: GDB:IL68T; GP130
A,Cross-references: GDB:126725; OMIM:600694
A,Map position: 5411-5411
C,Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.5%; Score 332; DB Best Local Similarity 37.1%; Pred. No. 4.4e-Matches 83; Conservative 28; Mismatches
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A;Cross-references: GDB:120315; OMIM:176761
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Best Local Similarity 28.2%
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A; Residues: 1-918 <HIB>
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                                                                                                                                                                                                          ASSACRATION RECEPTOR SHORT form Sla precursor, breast cancer cells T-47D - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Jacobation and characterization of two novel forms of the human prolactin recept A;Reference number: ASS405; MUID:21538812; PMID:11518703
A;Accession: ASS405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <HUI.>
A;Reference number: A94400
A;Reference number: A49400
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A;Residues: 1-376 <HUI.A;Residues: 1-376 <HUI.A;Residue
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: T-Uul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession. A40144; A57018
R;Boutin, J.M.; Edery, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D.;
Mol. Endocrinol. 3, 1455-1461, 1989
A;Title: Identification of a cDNA encoding a long form of prolactin receptor in human he A;Reference number: A40144; MUID:90114212; PMID:2558309
A;Accession: A40144
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 VHVSRVGGLEDQLSVRWV--SPPALKOF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: GDB:120315; OMIM:176761
A;Gene: GDB:120315; OMIM:176761
A;Gene: GDB:120315; OMIM:176761
A;Gep position: 5p13.3-5p13.1
C;Keywords: g1ycoprotein; transmembrane protein
C;Keywords: g1ycoprotein; transmembrane protein
C;Keywords: g1ycoprotein; transmembrane protein
C;Keywords: g1ycoprotein; transmembrane protein
C;Keywords: g1ycoprotein; transmembrane protein
C;Keywords: g1ycoprotein; transmembrane protein
C;Keywords: g1ycoprotein; receptor, short form S1a #status predicted
F;S5-376/Peroduct: gytokine receptor homology cGRS>
F;S5-376/Peroduct: gytokine receptor homology cGRS>
F;S9,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 338
       191 FKILSLHPGQKYLVQVRCKP-----DHGYWSAWSPATFIQIP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match

14.5%; Score 332; DB 2;
Best Local Similarity 37.1%; Pred. No. 2.4e-18;
Matches 83; Conservative 28; Mismatches 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 30-Apr-1993 #sequence_revision N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A;Fitle: Molecular cloning and characterization of the rat liver IL-6 signal transducin.
A;Reference number: A44257
A;Accession: A44257
A;Accession: A44257
A;Accession: preliminary; not compared with conceptual translation
A;Accessious: 1-918 *wANA
A;Residues: 1-918 *wANA
A;Cross-references: UNIPROT:P40190; UNIPARC:UP1000012D4D8
                                                                                                                                                                                                                                                                                                                                                                                                             A;Reaidues: 1-830 «CHE»
A;Cross-references: UNIPROT:Q90374; UNIPARC:UPI0000132233; EMBL:U07694; NID:g466381; PI)
P;36-220/Domain: cytokine receptor homology «CRSI»
P;240-426/Domain: cytokine receptor homology «CRSI»
                                                                                                                                                                                                                                                                     the pigeon prolactin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 SSVTPTDVVPQNVQLTCNILSFGQIEQNVYGITILSGYPPDIPTNLSCIVNEGKNMLCQL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 LALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRW 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 TPGAHGETFLHTNYSLKYKLRMYGQD-NTCEEYHTVGPHSCHIPKDLALFTPYEIWVEAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
                                                                                        prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Decies: 15-8pp-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150455
R;Chen, X.; Horseman, N.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPEKPTIIKCRSPEKETFTCWWKPGSDGG---HPTNYTLLYSKEGEERVYECPDYKTAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSCHI-PKDLALFTPYEIWVEATURLGSARSDVLTLDILDVVTTDPPPDV--HVSRVGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDQLSVRWVSPPALKDF - - - LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 IYPEFPVVQRGSNFTATCVLKEKCLQVY----SVNATYIVWKTNHVAVPKEQVTVINRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPEKPVNISCWSKNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 ISPODPTLLIGSSLLATC----SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%; Score 316; DB 2; Length 830 36.6%; Pred. No. 1.1e-16; ive 30; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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A;Note: sequence extracted fractor NCBI backbone (NCBIP:118488)
C;Keywords: transmembrane protein
F;134-315/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                   Endocrinology 135, 269-276, 1994
A/Title: Cloning, expression, and mutational analysis of
A/Reference number: IS0455; MUID:94283267; PMID:7516866
A/Accession: IS0455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                th 13.7%; Score 314.5; DB 2; Similarity 29.7%; Pred. No. 1.7e-16; 93; Conservative 51; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-6 signal transducing molecule gp130 - rat
                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 YFVQVRCNPFGIYGSKKAGIWSEWS 330
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Best Local Similarity 36.6%
Matches 75; Conservative
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Best Local Similarity
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Adcession: 148699; 148370
R;Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol: 148, 4066-4071, 1992
A;Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gpl3d
A;Title: Molecular Cloning of a murine IL-6 receptor-associated signal transducer, gpl3d
A;Reference number: 148370; MUID:92291532; PMID:1602143
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-917 <RES>
A;Cross-references: UNIPARC:UPI000002845A; GB:M83336; NID:g193591; PIDN:
A;Residues: 1-917 <RES>
A;Cross-references: UNIPARC:UPI00002845A; EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PI
C;Genetics:
C;Genetics:
A;Gene: gpl30
C;Keywords: gplycoprotein
F;134-314/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gp130
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FIDIASLANQLTCAILTFGQLEQAVYGITISGLPPEKPKALSCIVNEGKKARCEWDGGR 150
                                                                                                                                  --ETHLETNFTLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGK 206
                                                                                                                                                                                                                                                                                                                                                             265 DASTWSQIPPEDTASTRSSFTVQDLKPFTEXVFRIRC-----MKEDGKGYWSDWSERASG 319
                                                                                        HGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGS 218
                                                                                                                                                                                                        219 ARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKOFLFQAKYQIRYRVE 278
                                                                                                                                                                                                                                               DSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 LANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 PTDVVLPSVQLTCNILSFGQIEQNVYGVTMLSGFPPDKPTNLTCIVNEGKNMLCQWDPGR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 HGETFLHTNYSLKYKLRWYGQD-NTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 --ETYLETNYTLKSE--WATEKPPDČQSKHGT---SCMVSYMPTYYVNIEVWVEAENALG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 SARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 KVSSESINFDPVDKVKPTPPYNLSVTNSEELSSILKLSWVSSGL--GGLLDLKSDIQYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 ISPODPTLLIGSSLLATCSVHG---DPPGATAEGLYWTLNGRRLPPELSRVLNASTLALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.9%; Score 317.5; DB 2 29.6%; Pred. No. 9.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.9
Best Local Similarity 29.6
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 AST--PRSERP 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                            336 STPRSERP 343
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lactogen receptor 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Aocession: A34631
R;Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A;Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
A;Reference number: A34631; MUID:90241201; PMID:2159291
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*Residues: 1-610 <ZHA-
*Residues: 1-610 <ZHA-
*A;Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170BE1; GB:M34083; NID:g205122; PIDN
A;Note: the authors translated the codon GAG for residue 533 as Gly
F;31-216/Domain: cytokine receptor homology <CRS>
A;Reference number: 155417; MUID:95014432; PMID:7929319
A;Accession: 155417
A;Status: translated from GB/EMBL/DDBJ
A;Getus: translated from GB/EMBL/DDBJ
A;Residues: 1.412 cRES>
A;Cross-references: UNIPRRC:UPI00002819B; EMBL:U07567; NID:g641963; PIDN:AAA61784.1; A;Experimental source: Nb2-11C cell line
C;Keywords: transmembrane protein
F;31-216/Domain: cytokine receptor homology <CRS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 TYYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSSDPLYVDVTYIVEPEFP 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK
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35.0%; Pred. No. 1.3e-16;
ive 36; Mismatches 85; Indels
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Pred. No. 8.1e-17;
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35.0%;
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Matches 79; Conservative
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: A1070; I55417
Riali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 2010-2017; 1991
A; Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolact A; Patelerence number: A41070; MUID:92041834; PMID:1718958
A; Accession: A41070
A; Residues: I-412 AALI>
A; Residues: I-412 AALI>
A; Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19B; GB:M74152; NID:g206389; PIDN: R; O'Neal, K.D.; Yu-Lee, L.Y.
T; O'Neal, K.D.; Yu-Lee, L.Y.
T; Diol. Chem. 269, 26076-26082, 1994
A; Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prolactin receptor precursor - rat
prolactin receptor precursor - rat
C;Species: Rattus norregicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A29884
R;Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banville
Cell 53, 69-77, 1988
A;Title: Cloning and expression of the rat prolactin receptor, a member of the growth hc
A;Reference number: A29884; MUD:88165059; PMID:2832068
A;Accession: A29884
A;Accession: A29884
A;Residues: 1-310 eBOU>
A;Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19A; GB:M19304; NID:g206364; PIDN:
C;Keywords: transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-310/Product: prolactin receptor #status predicted <MAT>
F;31-216/Domain: cytokine receptor homology <CRS>
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                       147 DPGR--ETYLETNYTLKSE--WATEKFPDCRTKH--GISSCMMGYTPIYFVNIEVWVEAE
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35.0%; Pred. No. 5.7e-17;
tive 36; Mismatches 85.
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C; Species: Rattus norvegicus (Norway rat)
C; Date: 28 War-191
C; Date: 28 War-191
C; Date: 28 War-191
C; Date: 28 War-191
C; Date: 28 War-191
R; Shirota, M.; Barville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, J.
Mol. Endocrinol. 4, 1136-1143, 1990
A; Fitle: Expression of two forms of prolactin receptor in rat ovary and liver.
A; Reference number: A36116, MUID:91155946; PMID:2293022
A; Recession: A36116
A; Reference receives much a A36116
A; Residues: 1-610 < SH1>
A; Residues: 1-610 < SH1>
A; Cross-references: UNIPROT:P05710; UNIPARC:UP10000170ADB; GB:M57668; NID:g206366; PIDN: F;31-216/Domain: Cytokine receptor homology < CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B198; GB:M22959; NID:g200481; PIDN:
F;31-216/Domain: cytokine receptor homology <CRS>
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Cispecies: Mus muscrius (house mouse)
Cispecies: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
Cispecies: 01-77525
Ribavis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989
Mol. Endocrinol. 3, 674-680, 1989
Aritie: Expression of multiple forms of the prolactin receptor in mouse liver.
Areference number: 157699, MuID:89261824; PMID:2725531
Arecession: 177525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSSDFLYVDVTYIVEPEPP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 PDVHVSRVGGLEDQLSVRWV--SPPALKOF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 FTPYEIWVEATNRLGSARSDVLTLDILDVYTTDPPDVHVSRVGGLEDQLSVRWYS--PP 260
91 WKIXIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 LSRVLNASTLALALALANINGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT--CEEYHTVGPHSCHIPKD-LAL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 ALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PPGKPEIHKCRSP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 DKETFTCWMNPGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCPFSKQYTSI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prolactin receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I77525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.7%; Score 313; DB 2;
ilarity 35.0%; Pred. No. 1.3e-16;
Conservative 36; Mismatches 85
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Best Local Similarity
Matches 79; Conserv
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A;Accession: I77524
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-303 «FRES>
A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B197; GB:M22958; NID:g200479; PIDN
F;31-216/Domain: cytokine receptor homology «CRS»
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A; Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form A; Reference number: JT0671; MUID: 94085788; PMID: 8262385
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-608 < MOO>
A; Cross-references: UNIPARC: UPI000020E90; GB: L13593; NID: g347398; PIDN: AAC37641.1; PID R; Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
B; Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
A; Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
A; Reference number: S34356
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A;Residues: 1-608 <RES>
A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI000020E90; GB:L14811; NID:g293769; PIDN
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prolactin receptor, long form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
R;Clarke, D.L.; Linzer, D.I.H.
Endocrinology 133, 224-232, 1993
A;Title: Changes in prolactin receptor expression during pregnancy in the mouse owary.
A;Reference number: IS3269; MUID:93307149; PMID:8319571
                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor in mouse liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT--CEEYHTVGPHSCHIPKD-LAL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 FTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--PP 260
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                                                                                                                                                                                                     prolactin receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: 177524
R;Davis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989
A;Fille: Expression of multiple forms of the prolactin receptor in mouse liv
A;Reference number: 157699; MUID:89261824; PMID:2725531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%; Score 309.5; DB 2; Length 303; 31.4%; Pred. No. 1e-16;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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----DHGYWSRWGQEKSIEIP 222
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Best Local Similarity 31.44
Matches 82; Conservative
                              206
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: J01655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Bjochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA selectence number: J01655; MUID:93075121; PMID:1445292
A;Reference number: J01655
A;Reference number: J01655
A;Reference number: J01655
A;Residues: 1-81
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A;Accession: S34356
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A;Molecule type: mRNA
A;Residues: 1-557,'F','559-608 <EDE>
A;Residues: 1-557,'F','559-608 <EDE>
A;Cross-references: UNIPARC:UPI0000163B24; EMBL:X73372; NID:g312696; PIDN:CAA51789.1; PI
C;Comment: Prolactin receptor have long form and short form which are resulted from alte
C;Comment: This long form receptor is capable of transducing a signal to milk protein ge
C;Keywords: receptor; transmembrane protein
F;31-216/Domain: cytokine receptor homology <CRS>
F;230-253/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 ALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 317
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4.7e-16;
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Best Local Similarity 31.4%; Pred. No. 2.5e-16;
Matches 82; Conservative 38; Mismatches 94
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Search completed: April 11, 2006, 02:17:27 Job time: 22.0667 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 11, 2006, 02:04:23 ; Search time 125.397 Seconds (without alignments) 2368.694 Million cell updates/sec Run on:

US-09-037-657-44 2290 Title: Perfect score:

1 MPAGRRGPAAQSARRPPPLL.....NQDEGILPSGRRGTARGPAR 421 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Beq Beq 88 Minimum I Maximum I

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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۵	Query	Match	99.5	95.1	61.9	60.5	43.4	20.4	17.7	16.6	16.0	15.5	14.5	14.5	14.5	14.5	14.5	14.5	14.3	14.1	14.1	13.9	13.9	13.8	13.8	13.8	13.7	13.7	٠	٠	13.5	13.5	13.5
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ALIGNMENTS

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SPECIFICITY, AND INDUCTION.

TISSUB=Fetal lung;
MEDLINE=98349389; PubMed=986600;
Blson G.C.A., Graber P., Losberger C., Herren S., Gretener D.,
Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.-F.;
"CytoKine-like factor-1, a novel soluble protein, shares homology with members of the cytokine type I receptor family.";
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                      075462; Q9UHHS; 29-MAR-2004 (Rel. 43, Created) 29-MAR-2004 (Rel. 43, Last sequence update) 25-MAR-2005 (Rel. 48, Last annotation update) Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1) (CLP-1) (ZcytoRS).
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                                                                                  422 AA
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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Genome Res. 13:2265-2270(2003).
                                                                              STANDARD;
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NUCLEOTIDE SEQUENCE.
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SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)

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Attaubherg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Attaubherg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeebbrg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

Altschul S.F., Zeebbrg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Aspleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnhord P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Broak S.A., McKwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

Antilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Schwutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,

B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Mannes ChN. Sechein J.E., Jones Enalls D. Schill-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20423191; PubMed=10966616; DOI=10.1038/78765; BEDSON G.C.A., Lelievze B., Guillet C., Chevalier S., Plun-Favreau H., Froger J., Suard I., de Coignac A.B., Delneste Y., Bonnefoy J.Y., Gauchat J.-F., Gascan H., CLF, associates with CLC to form a functional heteromeric ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knappskog P.M., Majewski J., Livneh A., Nilsen P.T.E., Bringsli J.S.,
Ott J., Boman H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dtt J., Boman H.;
"Cold-induced sweating syndrome is caused by mutations in the CRLF1
                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN SEQUENCE OF 38-52.
PubMed=13340161, DOI=10.1110/ps.04682504;
Slang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally
                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [8]
VARIANTS CISS HIS-81 AND ARG-374.
MEDLINE=22428294; Pubmed=12509788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein Sci. 13:2819-2824 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the CNTF receptor complex.";
Nat. Neurosci. 3:867-872(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cleavage sites."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene.";
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J. Hum. Genet. 72:375-383(2003).

-!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory role in the immune system and during fetal development. May be involved in nervous system development.

-!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a heteromeric complex with cardiotrophin-like cytokine (CLC); the CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor receptor (CMTER).
SUBCELLULAR LOCATION: Secreted.
IISSUE SPECIFICITY: Highest levels of expression observed in spleen, thymus, lymph node, appendix, bone marrow, stomach, placenta, heart, thyroid and ovary. Strongly expressed also in

fetal lung.

INDUCTION: Up-regulated in fibroblast primary cell cultures under stimulation by IFV-gamma, TFV-alpha and IL-6.

SUMMIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.

SUMMIN: Defects in CRLF1 are the cause of cold-induced sweating syndrome (CISS) [MIM:272430]. CISS is an autosomal recessive disorder characterized by profuse sweating induced by cool surroundings (temperatures of 7 to 18 degrees Celsius). Additional abnormalities include a high-arched palate, nasal voice, depressed nasal bridge, inability to fully extend the elbows and kyphoscoliosis.

SIMILARITY: Belongs to the type I cytokine receptor family. Type 3 -

subfamily.
SIMILARITY: Contains 2 fibronectin type-III domains 1

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                 GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0019955; F:cytokine binding; IPI.
GO; GO:0019735; F:receptor activity; TAS.
GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
Pfam; PF00041; fn3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50835; IG_LIKE; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
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(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
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/FITIGVAR 0.17866.

240 D \rightarrow R (i\bar{n} Ref. 3).

46302 MW; AD9DEFCB01B84228 CRC64;
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Fibronectin type-III 1.
Fibronectin type-III 2.
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N-linked (GlCNAC.)
N-linked (GlCNAC.)
N-linked (GlCNAC.)
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N-linked (HCNAC.)
N-linked (HCNAC.)
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/FTId=VAR 017865.
L -> R (in CISS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WSXWS motif
                                                                                                                                            EMBL, AY3-8291, AAD54385.1; -; mRNA.
EMBL, AY3-8291, AAQ8658.1; -; mRNA.
EMBL, BC044634.1; -; mRNA.
HSSP, P40223; 1CD9.
Ensembl, ENSG00000006016; Homo sapiens.
                                                                                                                EMBL; AF05593; AAC28335.1; -; MENA.
EMBL; AF073515; AAD39681.1; -; MENA.
EMBL; AF178684; AAD54385.1; -; MENA.
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Potential.
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HSSP; P40223; 1CD9.
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94.8%;
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                                    LKPGTVYFVQVRCNPFG1YGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Defourtal mice.

SUBUNIT: Forms covalently linked di- and tetramers. Forms a heteromeric complex with cardiotrophin-like cytokine (CLC); the CREPI/CLC complex is a ligand for the ciliary neurotrophic factor receptor (CMTRR) (By similarity).

SUBCELLULAR LOCATION: Secreted (By similarity).

TISSUE SPECIFICITY: Widely expressed in the embryo. Not detected in the brain of adult mice.
VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
           241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                              LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                    GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the type I cytokine receptor family. Type
                                                                                                                                                                                              29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
29-MAR-2005 (Rel. 48, Last annotation update)
Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)
(Cytokine receptor-like molecule 3) (CRLM-3) (NR6).
Name-Crlfi; Synonyms-Crlm3;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                    Nicola N.A., Hilton D.J.; "Suckling defect in mice lacking the soluble haemopoietin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 2 fibronectin type-III domains. SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
                                                                                                                                                                                                                                                                                                                                                              PubMed=10359701; DOI=10.1016/S0960-9822(99)80266-8; Alexander W.S., Rakar S., Robb L., Farley A., Willson T.A., Zhang J.-G., Hartley L., Kikuchi Y., Kojima T., Nomura H., Hasegawa M., Macda M., Fabri L., Jachno K., Nash A., Metcalf
                                                                                                                                                                                                                                                                                                                           Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                        FUNCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. 9:605-608(1999)
                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                          (1)
NUCLEOTIDE SEQUENCE.
                                                                                                              421
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ATCSIHGDTPGATARGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALALANLNGSRQRSGDNLVCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 PPDVHVSRVGGLEDQLSVRMVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MPAGRRGPAAQSARRPP-PLLPL---LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVDVVTTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50853; FN3; 2.
PROSITE; PS50835; IG LIKB; FALSE NEG.
Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / similarity.
910535C629CA7056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytokine receptor-like
Ig-like C2-type.
Fibronectin type-III 1.
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Pred. No. 1.5e-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSXWS motif.
Phosphoserine.
N-linked (GlCNAc.)
N-linked (GlCNAc.)
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N-linked (GlCNAc.)
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MGI; MGI:1340030; Crlf1.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
Pfam; PF00041; fn3; 2.
SWART; SM00060; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
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NCBI_TaxID=99883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 GKRLPSSTYSILSPTVISVTLPRLSGSRQRSGDNLVCHNGGGHVLAGSCIYVGMPPEKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 LLPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPPGATAEGLYWTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MICLIFIHLCAAGVLSSSTQVATIYPQDPALLIGSSLTATCSVNPD-HGIHAGSLYWTLN
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                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 61.9%; Score 1418.5; DB 2; Length Local Similarity 67.6%; Pred. No. 2.4e-100; les 261; Conservative 50; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor; Repeat; Transmembrane.
SEQUENCE 389 AA; 43314 MW; E30903B99639864A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                             389 AA
                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50853; FN3; 2.
                                                                        QEDG28_BRARE PRELIMINARY;
QEDG28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
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SMART; SM00060; FN3; 2.
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                                                                                                                                                                                                                Zgc:91992.
ORFNames=zgc:91992;
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S:
Matches 261
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LEADY. The WSXMS motif appears to be necessary for protein folding and thereby efficient intracellular transport and cell-folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).

EMBL; AV374473; AAR25664 1; -; mRNA.

EMBL; AV374473; Tetracdon nigroviridis.

OR GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR002956; Cytkn recept_B/G.

InterPro; IPR003961; FN III.

INTERPRO; IPR00110; IG-like.

PROSITE; PS5083; IG-like.

RROSITE; PS5083; IG-LIKE; 1.

RROSITE; PS5083; IG-LIKE; 1.

WENCOSTE; PS5083; IG-LIKE; 1.

WENCOSTE; PS5083; IG-LIKE; 1.

WENCOSTE; PS5083; IG-LIKE; 1.

WENCOSTER; PS5083; IG-LIKE; 1.

SEQUENCE 394 AA; 44022 MW; EE60B16FA2C2896C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RA Dambed-15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bimmont C., Skalli Z., Cattolico L., Poulain J.-P., Berardinis Vd.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
Ralis M., Volff J.-N., Guigs R., Zody M.C., Mesirov J.,
Ralis M., Volff J.-N., Guigs R., Zody M.C., Mesirov J.,
Laudet V., Schachter V., Quitier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Crollius H.R.;
T. "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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DIALFTPYRIWVEATNRIGSARSDVLTLDILDVVTTDPPPDVHVSRVGCLEDQLSVRWVS 258
                                                                                                                                                                                                                                                                                                              GSKKKAGIWSEWSHPTAASTPRSERPGPGGACEPRGGEPSSGPVRRELKOFLGWLKKHAY 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                            180 DLALFTPYEIWVRASNQLGTATSDVIYLDILDVVTTDPPTDVIVSRVGDLEDQLTVRWGT
                                                                                                                                                                                                240 PPALKDFLFQAKYQIRYRLEBSSDWKVVDDVGNQTSCRLAGLRPGTVYFVQVRCNPVGIL
                                                                                                                                                                                                                                                                                                                                                           PPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFG1Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.5%; Score 1384.5; DB 2; Length 394; 67.6%; Pred. No. 9.7e-98; ive 41; Mismatches 78; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class I helical cytokine receptor number 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCSGMSIKLYDQWRVWLQKSHKTRNQ 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 -CSNLSFRLYDQWRAWMQKSHKTRNQ 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tetraodon nigroviridis (Green puffer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OGUAQS_TETING PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.5
Best Local Similarity 67.6
Matches 259; Conservative
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180 TSDVITLDILDVVTTDPPSGVTVSRVGQLEDQLSVRWEAPPALKDFLFQAKYQIRYRLED 239
                                                                                                                                                                                100 ANLAGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 SQDWKEBKSAFDQERERAWTEPLCILGLRVLMNBKYSVBAGFLQMALLRILLPVLWVMDD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 VGNOTSCRLAGIRPGTVYFVOV------GPRRSSASDRIWI-----SDRRV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSNQTSCRLAGLKPGTVYFVQVRCNPFG1YGSKKAG----IWSEWSHPTAASTPRSERPG 344
                                                                                          40 AVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALAL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruander G., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindbad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Guetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; Wichenen duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                  AVIYPODPVLRMGSNLTASCWIRSD-LGVHASSLFWTLNGOPLPSSLYRVLSPINLSVTL
                                                                                                                                                                                                           60 AGLNASRQTSGDNLVCHHKGHILAGSCLYVGMPPAKPVNLTCWSRNTKDLTCSWAPGGR
                                                                                                                                                                                                                                                                                                        QQVV-----
                                                                                                                                                                                                                                                                           GETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSA
                                                                                                                                                                                                                                                                                                                                                                      220 RSDVLTLDILDVVTTDPPPDVHVSRVGGLBDQLSVRWVSPPALKDFLFQAKYQIRYRVBD
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;

Butaryota, Neoplerygii, Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;

Tetradontoidea, Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-58F-2003 (itempares, 31, 2000 mms.comm. remov.)
Chromosome undetermined SCAP6801, whole genome shotgun sequence.
                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOCHINE SUBJECTION OF THE BUBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
  Length 437;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                               62;
43.4%; Score 994; DB 2;
53.8%; Pred. No. 9.8e-68;
                                             33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207
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Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORFNames=GSTENG00003230001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q4TCM7_TETNG PRELIMINARY;
Q4TCM7;
                       Best Local Similarity 53.8 Matches 199; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 PGGGACEPRG 354
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Query Match
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81
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Rarra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindbad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
McGonne duplication in the telecot fish Tetraodon nigroviridis reveals
LLLCVLGAPRA-GSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRR
                       LPPELSRVLNASTLALALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNIS
                                                                                                                  CWSKNWKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLA
                                                                                                                                                                                                                                                                         LPTPYRIWVEATURLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPA
                                                                                                                                                                                                                                                                                                   LKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAGIWSEWSHPTAASTPRSERPGPGGACEPRGGEPSSGPVRRELKQFLGWLKKHAY-CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetraodontoidea, Tetraodontidae, Tetraodon.
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FRB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
prellminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 10 SCAF15019, whole genome shotgun sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=GSTENG00031935001;
Tetraodon nigroviridis (Green puffer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMSMKLYDQWRVLMQKSHKARNQ 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 NLSFRLYDQWRAWMQKSHKTRNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q4RMPS_TETNG PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 431:946-957(2004)
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NON TER
SEQUENCE
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23
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Mauceli E., Bouneau L., Fischer S., Iutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Beraddinis V.,
Aruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Parra G., Larder G., Chaple C., McKernan K.J., McEwan P., Bosak S.,
Indblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E. S., Weissenbach J., Roest Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
II. Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 VITDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSN 291
                                                                                                                          ELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWS 144
                                                                                                                                                     74 STYGRLGPHTLSVTLHNINGSRQQSGDNLVCHSSDGHVLAGACLYVGMPPEKPVNLTCWS 133
                        LCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPP
                                                         20 VCV-----CGHHPDVAEVSPQDPVLPIGSSLTATCTLSPE-LRLLSSALYWTLNGETLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Etafinopterygii, Neopterygii, Taleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAPI5948, whole genome shotgun sequence.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 AA; 21734 MW; 299786CDFB24BDEB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                       199 AA.
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                                                                                                                                                                                                                                    145 KNMKDLTCRWTPGAHGET 162
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134 RNTKDLSCRWRPGGLGET 151
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Q4RDQ9;
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NUCLEOTIDE SEQUENCE.
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Arthouard C., Duprat S., Brottier P., Coulain J., De Berardinis V.,
A cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
A Rellis M., volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nubsuum C., Kahn D., Robinson-Rechavi M.,
A unicker P., Lander B., Weissenbach J., Roest Crollius H.;
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                    227 DILDOVOTTOPPPDVHVSRVGGLEDQLSVRWVSPPALKOFLFQAKYQIRYRVEDSVDWK-- 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------VVDDVSNQTSC 295
                                                                                                                                                                                                                                                                                                                                                                                               61 KSAFDQERERAWTEPLCILGLRVLMNEKYSVEAGPLQMALLRILLPVLWVMDDVGNQTSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----FVOVRCNPFGIYGSKKAGIWSEWSHPT 333
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis (Green puffer).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Eukaryota; Neopierygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF15947, whole genome shotgun sequence.
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                                                                                                                                                                                   73;
                                                                                                                                  Length 207;
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151 AA; 16177 MW; 14AD74333A6C7F90 CRC64;
                                                                            22607 MW; 71F8E80B9998309F CRC64;
                                                                                                                                                                                      28;
                                                                                                                               DB 2;
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                                                                                                                             Score 466.5; DB 2
Pred. No. 1.1e-27;
  CAAE01006801; CAF89355.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Mismatches
                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 AASTPRSERPGPGGGACEPRGGEPSSG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AASTPHSGEPPLPAGPGRSLGSAPESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                  20.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=GSTENG00037335001;
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                                                                                                                                                                                      Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 RLAGLKPGTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                   207 207 207 AA;
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                                                                                                                                                                                                                                                                                                                                                 285 -----
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Best Local Similarity
Matches 78; Conserv
                                                                                                                                  Query Match
Best Local Similarity
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EMBL; CA
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87

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NUCLEOTIDE SEQUENCE.
                                                                                                                                                Xenopodinae; Xen
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                                                                          Name=xgp130;
                                     01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMKDLTCRWTPGAHGETPLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 N----CTWNPGRH--TFLDTRFRLKYMWPRETFPDCIPEYVN---NSCTI-SDVQFFVN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 YEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDOLSVRWVSPPALKDF 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 LFQAKYQIRYRVEDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 VMELKFNIRYRISSDINWMEVPPEDIASPRISFSIQGLRPYTEYVFSIRC-----MKEDG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 ISPQDPTLLIGSSLLATCSVHG---DPPGATAEGLYWTLNGRRLPPELSRVLNASTLALA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 IIPESPVLALGSNFTALCILNESCLDFGNIYASQIIWKMKNKVIPKEQYREINRTVSSVT 93
                                                                                                                                                                                                                                                        TISSUE=Embryonic heart primary culture;
MEDLINE=99026068; PubMed=9806927;
Geissen M., Heller S., Pennica D., Ernsberger U., Rohrer H.;
Geissen M., Heller S., Pennica D., Ernsberger U., Rohrer H.;
"The specification of sympathetic neurotransmitter phenotype depends on gp130 cytokine receptor signaling.";
Development 125:4791-4801(1998).
-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).
-!- DOMAIN: The box I motif is required for JAK interaction and/or activation (By similarity).
EMBL, AJ011688; CAB42084.1; -; mRNA.
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 26 Potential.
918 AA; 102495 MW; FE7625FF3E3613EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 AGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------KPSKGP 334
                                                                          Last annotation update)
                                                    sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.0%; Score 365.5; DB 2; Best Local Similarity 30.1%; Pred. No. 3.9e-19; Matches 102; Conservative 44; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PP00041; fin3; 4.
Pfam; PP06328; Lep receptor Ig; 1.
SMART; SMO0060; FN3; 4.
PROSITE; PS06853; FN3; 5.
PROSITE; PS01353; HEMATOPO REC L F2; UNKNOWN 1.
918 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hemptrecept_1302.
InterPro; IPR010457; Lep_receptor_Ig.
                                     Created)
PRT;
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                                                        Last
                                 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                          Glycoprotein 130 precursor
O9W6U9 CHICK PRELIMINARY;
                                                                                                                           Gallus gallus (Chicken)
                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P40189; 1BQU
                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                           Name=gp130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311
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881 AA

PRT;

O57519 XENLA PRELIMINARY, 057519;

XENLA

RESULT 10 057519 XEN ID 05751 AC 05751

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61 VHGDPPGAT------AEGLYWTLNGRRLPPELSRVLNASTLALALALANINGSRQR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 SETLTIDPUNIVKPNPPQLSELISSLELPNALKIEWKNPIT---NAFNLKYNIRYRPVKT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 TLSH--RWAHFGANYCRGANNSC-----TIHSP-GFQFYIDTTFQVRATNELGIQK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 VDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAST 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 QDWEMVPEEDTASHRDSFTLQDLLPNTVYEVSIRC----IHKDGHGFWSDWSELKKQVT 314
                                                                                                                                                                                                                                                                                                                                          Chen J., Grace A., Chien K.R.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- DOWAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).
-!- DOWAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Prolactin receptor delta 7/11.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLKYKLRW-----YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 SGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoldea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 354; DB 2; Length 881; Pred. No. 2.9e-18; 41; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               881 AA; 99003 MW; 7DE7942D211138A0 CRC64;
(TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50853; FN3; 5.
PROSITE; PS01353; HEMATOPO REC L F2; UNKNOWN 1.
Receptor; Repeat; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003529; Hemptrecept_1302.
InterPro; IPR010457; Lep_receptor_Ig.
Pfam; PF000041; fn3; 4.
Pfam; PF06528; Lep_receptor_Ig; 1.
SWART; SM00060; FN3; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 PRSERPGPGGGACEPRGGEPSSGP 361
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HSSP; P40189; 1BJ8.
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                                                                                                                                                                                                                                     Xenopus; Xenopus
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Q8TD78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 30.2
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            081078
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Receptor.
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Q9UHJ5 HUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 294
                                                                                                                                                                                                                                                                                                                           Ensembl; ENSC0000113494; Homo sapiens.
Ensembl; ENSC0000113494; Homo sapiens.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004892; F:hematopoietin/interferon-class (D200-domain. .; IEA.
GO; GO:0004892; F:hematopoietin/interferon-class (D200-domain. .; IEA.
InterPro; IPR002996; Cytkn_recept_B/G.
InterPro; IPR003501; FN III.
InterPro; IPR003528; HemptreceptL_F1.
Pfam; PR00041; fin3; 2.
SMART; SM00060; FN3; 2.
                                                                                                       Trott J.F., Hovey R.C., Koduri S., Vonderhaar B.K.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-! DOMAIN: The WAXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).
-!- DOMAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 NICEEYHIVGPHSCHIPKO-LALFIPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 FKILSLHPGQKYLVQVRCKP-----DHGYWSAWSPATFIQIPSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trott J.F., Hovey R.C., Vonderhaar B.K.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 AA; 30705 MW; FBB498AB649A078C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 14.5%; Score 333; DB 2; 1 Similarity 36.6%; Pred. No. 2.7e-17; 83; Conservative 29; Mismatches 97,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSS0853; FN3; 2.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
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                                                                                                                                                                                                                                                               EMBL; AF492470; AAM18048.1; -; mRNA.
HSSP; P16471; 1BP3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96P36 HUMAN PRELIMINARY;
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                                                                                         TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
PubMed=11518703;
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                                                                  NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
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HUMAN
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Matches
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1. Biol. Chem. 276:41086-41094(2001).

2. John Chem. 276:41086-41094(2001).

2. John Chem. 276:41086-41094(2001).

3. Biol. Chem. 276:41088 motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).

3. Colding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).

3. Colombia.

3. EMBL; AF416618; AAL23914.1; -; mRNA.

3. RSP P18; B59405; B59405.

3. RSP P18; B59405; B59405.

3. RSP P18; B59405; B59405.

3. RSP P18; B59405; B7 RSP P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18; B7 P18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=20054419; PUDMed=10585417; DOI=10.1074/jbc.274.50.35461;
Kline J.B., Roehrs H., Clevenger C.V.;
*Runctional characterization of the intermediate isoform of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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J. Biol. Chem. 274-35468 (1999).
-1- DOWAIN: The WSXWS motif appears to be necessary for proper prote folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).
-1- DOWAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).
Hu Z.Z., Meng J., Dufau M.L.;
"Isolation and characterization of two novel forms of the human prolactin receptor generated by alternative splicing of a newly identified exon 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 AA; 32760 MW; B45203EC045EB417 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83; Conservative
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folding and thereby efficient intracellular transport and cell-
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PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 294
                                                                                                                                                                             NAS.
                                                                                                                                                                                                                                                                     .; IDA.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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GO; GO:0049278; F:crnithine decarboxylase activator activity; NAS.

R GO; GO:004925; F:protein homodimerization activity; NAS.

R GO; GO:0004925; F:protein homodimerization activity; NAS.

GO; GO:0007166; P:cell surface receptor linked signal transdu. .; NW

R GO; GO:0007166; P:cell surface receptor linked signal transdu. .; NW

R GO; GO:0007595; P:lactroin, NAS.

R GO; GO:0007110; P:r-cell activation; NAS.

R GO; GO:0007110; P:r-cell activation; NAS.

R GO; GO:000717; P:ransmembrane receptor protein tyrosine kin. .; II

R GO; GO:000717; P:ransmembrane receptor protein tyrosine kin. .; II

R GO; GO:000717; P:ransmembrane receptor protein; NAS.

R InterPro; IPR002996; Cytkn recept_B/G.

R InterPro; IPR003961; FN III.

R InterPro; IPR003561; FN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Gaps
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Hu Z.Z., Meng J., Dufau M.L.;
Igolation and characterization of two novel forms of the human prolactin receptor generated by alternative splicing of a newly identified exon 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 FKILSIHPGQKYLVQVRCKP-----DHGYWSAWSPATFIQIP 227
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 AA; 39806 MW; 932F200E850CDD27 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.5%; Score 332; DB 2; 37.1%; Pred. No. 4.4e-17; iive 28; Mismatches 95,
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PROSITE; PS50853; FN3; 2.
PROSITE; PS01352; HEWATOPO_REC_L_F1; 1.
  EMBL; AF166329; AAD49855.1; -; mRNA.
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Q96P35;
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122 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 180
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utiface receptor binding (By similarity).

"I DOWAIN: The box 1 motif is required for JAK interaction and/or activation (By similarity).

EMBL; AP416619; AAL23915.1; -; mRNA.

BR R; AS9405; AS9405.

BR R; AS9405; AS9405.

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDIATE=90114212; PubMed=258309;
BOUTINE=90114212; PubMed=258309;
BOUTIN J.-M., Edery M., Shirota M., Jolicoeur C., Lesueur L., Ali S.,
Gould D., Djiane J., Kelly P.A.;
"Identification of a cDNA encoding a long form of prolactin receptor
in human hepatoma and breast cancer cells.";
Mol. Endocrinol. 3:1455-1461(1989).
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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DOMAIN: The box 1 motif is required for JAK interaction and/or
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MIM; 176761; -.
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SIGNAL 1 2
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 MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Bapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Ndckernan K.J., Malek J.A., Gunaratne P.H., Richards S.M., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.W., Willahy K.J., Hallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willaho D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Reference C.M., Aschein J.B., Jones S.J.M., Marra M.A.; Reference C. M. Smailus D.E., Grimwood J., Schmutz J., Myers R.M., Touchman J.W., Green E.D., Dickson M.C., Schein J.E., Jones S.J.M., Marra M.A.; Reference C.M., Smailus D.E., Grimwood J., Schmutz J., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Touchman J.W., Green E.D., Myers R.M., Myer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.
MEDLINE=95075462; PubMed=7984244; DOI=10.1038/372478a0;
Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;
"The X-ray structure of a growth hormone-prolactin receptor complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P16471-3; Sequence=VSP 012620, VSP 012621;
Note=Soluble isoform that appears specific for the BT-474 breast
cancer cell line;
                                                                                                                                                                        Kline J.B., Clevenger C.V.; "Characterization of a novel and functional human prolactin receptor isoform (delta-S1 PRLr) containing only one extracellular fibronectin-
              NUCLEOTIDE SEQUENCE (ISOFORM 1).
MEDIINE=99182102; PubMed=10084611; DOI=10.1210/jc.84.3.1153;
Hu Z.-Z., Zhuang L., Meng J., Leondires M., Dufau M.L.;
"The human prolactin receptor gene structure and alternative promoter utilization: the generic promoter hPIII and a novel human promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 372:478-481(1994).
-!- FUNCTION: This is a receptor for the anterior pituitary hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Mammary carcinoma;
MEDILINE=9528659; PubMed=7768908; DOI=10.1074/jbc.270.22.13133;
Fuh G., Wells J.A.;
"Prolactin receptor antagonists that inhibit the growth of breast
cancer cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P51956:NEK3; NDEXP=1; INLACt=EBI-476182, EBI-476041; P52735:VAV2; NDEXP=1; INLACt=EBI-476182, EBI-297549; -i- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                      Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=3;
                                                                                                            Clin. Endocrinol. Metab. 84:1153-1156(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=2; Synonyms=Delta-S1;
IsoId=P16471-2; Sequence=VSP_001720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P16471-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 270:13133-13137(1995).
                                                                                                                            [3]
NUCLEOTIDE SEQUENCE (ISOFORM 2)
                                                                                                                                                           TISSUE=Mammary carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prolactin.
INTERACTION:
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                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
activation. SHOOMS to the type I cytokine receptor family. Type 1
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PROSITE; PS50853; FN3; 2.
PROSITE; PS01352; FN3; 2.
3D-structure; Alternative Fplicing; Glycoprotein; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Potential).
                                                                                                                                                                   -!- SIMILARITY: Contains 2 fibronectin type-III domains.
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By similarity.
Missing (in isoform 2).
/FTIG=VSP 001720.
DF -> AW (in isoform 3).
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Missing (In isoform 3).
/FTId=VSP 012621.
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N-linked (GlcNAc. ..)
N-linked (GlcNAc. ..)
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EMBL; AF091863; AAD32032.1; -; Genomic_DNA.
EMBL; AF091864; AAD32032.1; JOINED; Genomic_DNA.
EMBL; AF091865; AAD32032.1; JOINED; Genomic_DNA.
EMBL; AF091866; AAD32032.1; JOINED; Genomic_DNA.
EMBL; AF091866; AAD32032.1; JOINED; Genomic_DNA.
EMBL; AF091869; AAD32032.1; JOINED; Genomic_DNA.
EMBL; AF091869; AAD32032.1; JOINED; Genomic_DNA.
EMBL; AF091869; AAD32032.1; JOINED; Genomic_DNA.
EMBL; AF091869; AAD32032.1; JOINED; Genomic_DNA.
EMBL; RC059392; AAB32032.1; -; mRNA.
EMBL; SC059392; AAB45392.1; -; mRNA.
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PDB; IBP2; X-Tay; B=25-235.
Intact; P16471; Bisembl; ENSG0000113494; Homo sapiens.
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Best Local Similarity 37.1%; Pred. No. 9e-17;
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111 11103333333333333333333333333333333	ULT 1 09-866-028-32 equence 32, Application US/09 atent No. 6642560 atent No. 6642160 APPLICANT: Baker, Kevin APPLICANT: Besterin, David APPLICANT: Betstein, David APPLICANT: Gerrara, Napoleone APPLICANT: Ferrara, Napoleone APPLICANT: Gerritsen, Mary APPLICANT: Gerritsen, Mary APPLICANT: Grandard, Audrey APPLICANT: Grimaldi, Christop APPLICANT: Grimaldi, Christop APPLICANT: Grimaldi, Christop APPLICANT: Hillan, Kenneth APPLICANT: Hillan, Kenneth APPLICANT: Hillan, Kenneth APPLICANT: Napier, Mary APPLICANT: Napier, Mary APPLICANT: Nood, William TITLE OF INVENTION: SECRETED TITLE OF INVENTION: SECRETED TITLE OF INVENTION: ACIDE EN TITLE OF INVENTION SECRETED CURRENT FILING DATE: 2001-05 EVIOL APPLICATION NUMBER: U CURRENT FILING DATE: 2010-05 EVIOL APPLICATION NUMBER: U CURRENT FILING DATE: 2010-05 EVIOL APPLICATION NUMBER: U CURRENT FILING DATE: 2010-05 EVIOL APPLICATION NUMBER: U CURRENT FILING DATE: 2010-05 EVIOL APPLICATION NUMBER: U TYPE: PRT ORGANISM: Home Sapien	99. larity 99. Conservative GRRGPAAQSARR
	Application A42360 A42160 A42160 A42160 A42160 A42160 A42160 A42160 A42160 Bacerin, Dav Berein, Dav Berein, Dav Berein, Dav Gerritsen, Mapo Gedowski, Pau Grilavin, Ivar Hillan, Kenne Hillan, Kenne Hillan, Kenne Hillan, Kenne Kodowski, Pau Gerritsen, Mary Roy, Margaret Roy, Margaret Roy, Margaret Roy, Margaret Collavious SECR ENTION: ACI CENTION: SECR ENTION: ACI CENTION: SECR ENTION: ACI CENTION: SECR ENTION: ACI CENTION:	PA B BY
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SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD

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Sequence Sequence Sequence Sequence

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120 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 179
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Pred. No. 1.2e-210;
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OR FILING DATE: September 15, 1999
OR PILING DATE: No. 6734288ember 30, 1999
OR APPLICATION NUMBER: PCT/US99/28313
OR FILING DATE: No. 6734288ember 30, 1999
OR FILING DATE: December 1, 1999
OR FILING DATE: December 1, 1999
OR FILING DATE: December 1, 1999
OR FILING DATE: December 16, 1999
OR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR PILING DATE: February 9, 1998
PRIOR PLILING DATE: February 9, 1998
PRIOR PLILING DATE: February 9, 1998
PRIOR PLILING DATE: February 25, 1998
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PRIOR PLILING DATE: NO. 673428ember 30, 199
PRIOR PLILING DATE: PECHUS99/289/30095
PRIOR PELICATION NUMBER: PCT/US99/28301
PRIOR PLILING DATE: PEDCEMBER 1, 1999
PRIOR PLILING DATE: PEDCEMBER 1, 1999
PRIOR PLILING DATE: PEDCEMBER PCT/US00/0569
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PRIOR PLILING DATE: PEDLUARY 22, 2000
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Best Local Similarity 99.8%;
Matches 421; Conservative (
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CORGANISM: Homo Sapien
US-09-944-457-32
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MOCOL, WILLIAM:
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P248PICI
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: December 3, 1997
PRIOR FILING DATE: December 1, 1997
PRIOR FILING DATE: December 1, 1997
PRIOR FILING DATE: December 11, 1997
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                180 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 239
                                                       181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVITLDILDVVTTDPPPD 240
                                                                                                                                        240 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 299
                                                                                                                                                                                                                                                                 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 359
                                                                                                                                                                                                                                                                                                                     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSFWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
                                                                                                                                                                                                                                                                                                                                                                                          GPVRRELKQFLGWLKKHAYCSNLSPRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
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PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
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FILING DATE: December 18, 1997
PAPLICATION NUMBER: 60/070,440
FILING DATE: January 5, 1998
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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APPLICANT: Botstein, David
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Goddard, Audrey
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Napier, Mary
Roy, Margaret
Tumas, Daniel
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PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR PLILING DATE: February 9, 1998
PRIOR PLILING DATE: February 2, 1998
PRIOR FILING DATE: February 2, 1998
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PRIOR PILING DATE: December 1, 1999
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PRIOR PILING DATE: PEDITORION NUMBER: PCT/US99/28301
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: PEDITORION NUMBER: PCT/US09/0414
PRIOR PILING DATE: PEDITORION NUMBER: PCT/US09/0414
PRIOR PILING DATE: PEDITORION NUMBER: PCT/US09/0414
PRIOR PILING DATE: PEDITORION NUMBER: PCT/US00/0414
PRIOR PILING DATE: PEDITORION NUMBER: PCT/US00/0414
PRIOR PILING DATE: PEDITORION NUMBER: PCT/US00/0501
PRIOR PILING DATE: MAY 22, 2000
PRIOR PILING DATE: MATCH 30, 2000
PRIOR PILING DATE: MATCH 30, 2000
PRIOR PILING DATE: PEDITORION NUMBER: PCT/US00/0501
PRIOR PILING DATE: PEDITORION NUMBER: PCT/US00/0501
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Best Local Similarity 99.8
Matches 421; Conservative
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SEQ ID NO 32
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ORGANISM: Homo Sapien
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APPLICANT: Napler, Mary
APPLICANT: Napler, Mary
APPLICANT: Napler, Mary
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Milliam
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
CURRENT APPLICATION NUMBER: US/09/945,584
CURRENT FILING DATE: 2001-09-26
PRIOR PLING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/66/411
PRIOR APPLICATION NUMBER: 60/66/411
PRIOR APPLICATION NUMBER: 60/66/335
PRIOR PLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/66/278
PRIOR APPLICATION NUMBER: 60/66/278
PRIOR APPLICATION NUMBER: 60/66/278
PRIOR PLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/66/278
PRIOR PLING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/66/278
PRIOR PLING DATE: December 16, 1997
PRIOR PLING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/66/9702
PRIOR PLING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/66/9702
PRIOR PLING DATE: December 17, 1997
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PRIOR PLING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/66, 917
                                         240 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 299
                                                                                                                                                                    241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
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         DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 239
                                                                                                                                                                                                                                                        300 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 359
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Grimaldi, Christopher
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Goddard, Audrey
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Hillan, Kenneth
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APPLICANT: Numbal, Juliana, Paplicant:
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION NUMBER: US/09/44,944

CURRENT FILING DATE: 2001-09-26
PRIOR PLILOR DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/69,334
PRIOR PLILING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 12, 1997
PRIOR PLILING DATE: December 12, 1997
PRIOR PLILING DATE: December 12, 1997
PRIOR PLILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/69,425
PRIOR PLILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,437
PRIOR APPLICATION NUMBER: 60/069,437
PRIOR APPLICATION NUMBER: 60/069,637
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR APPLICATION NUMBER: 60/069,873
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                                      DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                              241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                                                                                                                                                                                                           LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGACEPRGGEPSS
                                                                                                                                                                                                                                                            301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERFGPGGGACEPRGGEPSS
DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
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APPLICATION NUMBER: 60/070,440
FILING DATE: January 5, 1998
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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Filvaroff, Ellen
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APPLICANT: Baker, Kevin
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Goddard, Audrey
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Roy, Margaret
Tumas, Daniel
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99.5%; Score 2279.5; DB 2
Best Local Similarity 99.8%; Pred. No. 1.2e-210;
Matches 421; Conservative 0; Mismatches 0;
       IOR FILING DATE: February 9, 1998

IOR APPLICATION NUMBER: 60/074,092

IOR FILING DATE: February 9, 1998

IOR APPLICATION NUMBER: 60/075,945

IOR FILING DATE: February 25, 1998

IOR FILING DATE: December 16, 1998

IOR PELLING DATE: December 16, 1998

IOR APPLICATION NUMBER: 60/113,296

IOR APPLICATION NUMBER: 60/146,222

IOR PELLING DATE: December 22, 1998

IOR APPLICATION NUMBER: PCT/US98/19330

IOR PELLING DATE: December 16, 1998

IOR PELLING DATE: December 16, 1998

IOR PELLING DATE: December 16, 1998

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IOR PELLING DATE: December 16, 1998

IOR PELLING DATE: DECEMBER: PCT/US99/2252

IOR PELLING DATE: March 3, 1999

IOR PELLING DATE: March 3, 1999

IOR PELLING DATE: September 130, 1999

IOR PELLING DATE: September 15, 1999

IOR PELLING DATE: September 15, 1999

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IOR PELLING DATE: NOW BER: PCT/US99/28331

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IOR PELLING DATE: NOW BER: PCT/US99/28331
FRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: Pebruary 9, 1998
PRIOR FILING DATE: Pebruary 9, 1998
PRIOR FILING DATE: Pebruary 25, 1998
PRIOR APPLICATION NUMBER: 60/012,850
PRIOR PRILING DATE: Pebruary 25, 1998
PRIOR PILING DATE: December 12, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 12, 1998
PRIOR FILING DATE: December 16, 1998
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PRIOR FILING DATE: DECEMBER: 09/218, 311
PRIOR FILING DATE: DECEMBER 167/US99/28313
PRIOR FILING DATE: DECEMBER 16, 1999
PRIOR FILING DATE: DECEMBER 16, 1999
PRIOR FILING DATE: DECEMBER 16, 1999
PRIOR FILING DATE: NO. 692947 ember 30, 1999
PRIOR FILING DATE: PECTIVUS99/03565
PRIOR FILING DATE: PECTIVUS99/0369
PRIOR FILING DATE: PEDCHAARY 11, 2000
PRIOR PILING DATE: PEDCHAARY 11, 2000
PRIOR PILING DATE: PEDCHAARY 11, 2000
PRIOR FILING DATE: PEDCHAARY 11, 2000
PRIOR PILING DATE: PEDCHAARY 11, 2000
PRIOR FILING DATE: PEDCHAARY 11, 2000
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ORGANISM: Homo Sapien
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60 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANINGSRQRSGDNLVCHARD 119
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                                                                                                                                                                                                                                                                                                                                                                                                   IOR FILING DATE: September 16, 1998

IOR APPLICATION NUMBER: PCT/US98/19330

IOR APPLICATION NUMBER: PCT/US98/25108

IOR FILING DATE: December 16, 1998

IOR PILING DATE: December 16, 1998

IOR PILING DATE: December 22, 1998

IOR APPLICATION NUMBER: 09/218,517

IOR FILING DATE: March 3, 1999

IOR PELING DATE: March 3, 1999

IOR PELING DATE: March 3, 1999

IOR FILING DATE: March 3, 1999

IOR FILING DATE: PCT/US99/1252

IOR APPLICATION NUMBER: PCT/US99/28409

IOR FILING DATE: September 15, 1999

IOR PILING DATE: No. 6936254ember 30, 1999

IOR PELING DATE: No. 6936545ember 30, 1999

IOR PELING DATE: No. 693654ember 30, 1999

IOR PILING DATE: No. 693654ember 30, 1999

IOR PILING DATE: December1, 1999

IOR PELING DATE: December 16, 1999

IOR PELING DATE: DECEMBER: PCT/US99/30055

IOR PELING DATE: DECEMBER: PCT/US99/30055
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 25, 1998
PRIOR FILING DATE: February 25, 1998
PRIOR FILING DATE: Peocember 16, 1998
PRIOR FILING DATE: Peocember 16, 1998
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: DECEMBER 19, 1999
PRIOR FILING DATE: DECEMBER 19, 1999
PRIOR FILING DATE: DECEMBER 16, 1999
PRIOR FILING DATE: NO. 6936254ember 30, 1999
PRIOR FILING DATE: NO. 6936254ember 30, 1999
PRIOR FILING DATE: NO. 6936254ember 30, 1999
PRIOR FILING DATE: NO. 6936254ember 30, 1999
PRIOR FILING DATE: PEDCEMBER 19, 2000
PRIOR APPLICATION NUMBER: PCT/US99/2031
PRIOR FILING DATE: PEDCEMBER 16, 1999
PRIOR FILING DATE: PEDCEMBER 16, 1999
PRIOR FILING DATE: PEDCEMBER 16, 1999
PRIOR FILING DATE: PEDCEMBER 16, 1999
PRIOR FILING DATE: PEDCEMBER 16, 1999
PRIOR FILING DATE: PEDCEMBER 16, 1999
PRIOR FILING DATE: PEDCEMBER 19, 20, 2000
PRIOR PRILING DATE: PEDCEMBER 19, 20, 2000
PRIOR PRILING DATE: PEDCEMBER 19, 2000
PRIOR PRILING DATE: PEDCEMBER 19, 2000
PRIOR PRILING DATE: PEDCEMBER 19, 2000
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PRIOR PRILING DATE: PEDCEMBER 19, 2000
PRIOR PRILING DATE: PEDCEMBER 19, 2001
PRIOR PRILING DATE: PEDCEMBER 19, 2001
PRIOR PRILING DATE: PEDCEMBER 17, 2000
PRIOR APPLICATION NUMBER: PCT/US00/2018
PRIOR PRILING DATE: PEDCEMBER 19, 2000
PRIOR APPLICATION NUMBER: PCT/US00/2018
PRIOR PRILING DATE: PEDCEMBER 10, 2000
PRIOR APPLICATION NUMBER: PCT/US00/2018
PRIOR PRILING DATE: PEDCEMBER 10, 2000
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ORGANISM: Homo Sapien
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CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR PELING DATE: 1001-06-26
PRIOR PELING DATE: December 3, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 12, 1997
PRIOR PELING DATE: December 12, 1997
PRIOR PELING DATE: December 16, 1997
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PRIOR PELING DATE: DECEMBER: 60/669, 694
PRIOR PELING DATE: DECEMBER: 60/669, 694
PRIOR PELING DATE: DECEMBER: 60/669, 694
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PRIOR PELING DATE: DECEMBER: 60/669, 697
PRIOR PELING DATE: DECEMBER: 60/669, 697
PRIOR PELING DATE: DECEMBER: 60/669, 697
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PRIOR PELING DAT
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                                                   VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
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Patent No. 6936254
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Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Hillan, Kenneth
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Goddard, Audrey
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Tumas, Daniel
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US-09-945-587-32
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                                                                  240 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 299
                                                                                                                                                                                                                       361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                  181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                     241 VHVSRVGGLEDQLSVR#VSPPALKDFLFQAKYQIRYRVEDSVD#KVVDDVSNQTSCRLAG
                                                                                                                                   300 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                                                    360 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
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APPLICATION NUMBER: US/09/071,224
                                                                                                                                                                                                                                                                                                                                                                            Sequence 2. Application US/09071224
Patent No. 6271343
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Jelmberg, Anna C.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MANMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Zymogenetics
1201 Eastlake Ave East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFFCATION:
PRIOR APPLICATION:
APPLICATION NUMBER:
ATTONNEY, AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFRERENCE/DOCKET NUMBER: 96-22
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 206-442-6678
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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ADDRESSEE: Zymogenet
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CITY: Seattle
STATE: WA
COUNTRY: USA
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Length 422;

DB 2;

Score 2275.5;

99.48;

Query Match

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SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 119
                                                                                                                                                           120 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFILHTNYSLKYKLRWYGQ 179
                                                                                                                                                                                                                                   240 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 299
                                                                                                                                                                                                                                                                                                                                                                                       241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                             LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                             DNTCEBYHTVGPHSCHI PKDLALFTPYBIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                       1 MPAGRRGPAAQSARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
               Gaps
                 Indels
99.5%; Pred. No. 2.9e-210; cive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEC for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dresnell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Roster, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-071-224-4
; Sequence 4, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 98102
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMpatible
OPERATING SYSTEM: DOS
                     420; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Sequence 6, Application US/09071224

Patent No. 6271343

GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Presnell, Scott R.
APPLICANT: Jeliberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Adama, Robyn L.
AAPPLICANT: Adama, Robyn L.
AAPPLICANT: Adama, Robyn L.
AAPPLICANT: Adama, Robyn L.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
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ER: 96-22
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,79
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SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
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CORRESPONDENCE ADDRESS
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US-09-071-224-6
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APPLICANT: Timans, Jacqueline C.
APPLICANT: Kastelein, Robert A.
APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
FILE REFERENCE: DX0935K
CURRENT APPLICATION NUMBER: US/09/521,335
CURRENT PILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                          Query Match 95.9%; Score 2196; DB 2; Length 425; Best Local Similarity 100.0%; Pred. No. 1.3e-202; Matches 403; Conservative 0; Mismatches 0: Indels
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Sequence 12, Application US/09521335
Patent No. 6800460
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                           INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
STRANNBDNESS: single
TOPOLOGY: linear
                  TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
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Best Local Similarity 98.88
Matches 405; Conservative
                                                                                                                                                                                                   MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: primate US-09-521-335-12
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LENGTH: 410
TYPE: PRT
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121 GSILAGSCLYVGLPPEKPVNISCWSKNMKOLICRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
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                                                                                                                                     61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVINASTLALALANINGSRQRSGDNLVCHARD 120
                                                                                                                                                                                                                           120 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 359
360 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
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CITY: Seattle
STATE: WA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/071,224
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FIPYEIWVEATURLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPAL 246
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                                            SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
                          GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 179
                                                                                                                                                                                                                                                         PRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKS 397
                                                                                                                                                                                                                                                                     PSELSRILINTSTIALALALANINGSRQOSGDNLVCHARDGSILAGSCLYVGLPPBKPFNISC
                                                                                                 241 PATPGLSLIVRGKVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 PPELSRVINASTLALALANINGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISC
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                                                                                                                                         -----VVITTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRV
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                                                                                  DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILD-----
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Patent No. 6060276
GENERAL INFORMATION:
APPLICANT: MARSIAKOWSKI, PIOLT
ITLE OF INVENTION: No. 6060276e1 Orphan Rec
PILE REFERENCE: REG 630
CURRENT APPLICATION NUMBER: US/09/012,072
CURRENT FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity
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ORGANISM: MOUSE
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US-09-012-072-2
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US-09-012-072-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGAA 420
                                                                                                                                                                                                                   61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALALANLNGSRQQSGDNLVCH 120
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                                                                                                                                                                                                                                                           117 ARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 176
                                                                                                                                                                                                                                                                                                                                                                           PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 296
                                                                                                                                                              1 MPAGRRGPAAQSARRPP----PLLPLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MPAGRRGPAAQSARRPPPLLPLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
                                                                                                                                                                                                                                                                                                                    YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDP
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                                                                                     Length 425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION MASSIANOWSKI, Piotr
TITLE OF INVENTION: No. 6207413el Orphan Receptors
FILE REFERENCE: REG 630
CURRENT APPLICATION NUMBER: US/09/120,601
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: 09/012,072
NUMBER OF SEQ ID NOS: 6
                                                                                                                   15;
                                                                                     Score 2165; DB 2;
Pred. No. 1.3e-199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2164.5; DB 2
Pred. No. 1.5e-199;
                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09120601
Patent No. 6207413
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.5%;
94.6%;
                                                                                    94.5%;
Local Similarity 94.1%;
hes 399; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403; Conservative
  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 403; Conserv
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; ORGANISM: HUMAN
US-09-120-601-6
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US-09-071-224-6
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Matches
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RESULT 14
US-09-521-335-13
Sequence 13, Application US/09521335
Patent No. 6800460
GENERAL INFORMATION:
 Zymogenetics
)1 Bastlake Ave Bast
                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.5
Matches 386; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                     STREET: 1201 E
CITY: Seattle
                   1201
                                                                       USA
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 ADDRESSEE:
                                                                                          98102
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US-09-071-224-17
                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 WSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLAL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKK 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGIWSEWSHPTAASTPRSERPGPGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNL 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 405;
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                                                                                                                                                       GENERAL INCORMATION:
APPLICANT: Masiakowski, Piotr
APPLICANT: Masiakowski, Piotr
TITLE OF INVENTION: NO. 6207413el Orphan Receptors
FILE REPERENCE: REG 630
CURRENT APPLICATION NUMBER: US/09/120,601
GURRENT FILING DATE: 1998-07-22
BARLIER PELLOATION NUMBER: 09/012,072
BARLIER FILING DATE: 1998-01-22
NUMBER: OF SEQ ID NOS: 6
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 2
383 SFRLYDOWRAWMOKSHKTRNODEGILPSGRRGTARGPA 420
                       367 SFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGAARGPA 404
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Best Local Similarity 96.5%; Pred. No. 2.9e-194;
Matches 384; Conservative 5; Mismatches 9;
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Patent No. 6271343

GENERAL INFORMATION:
APPLICANT: Dick, Si
APPLICANT: Defaberg, Anna C.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Adams, Robyn L.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                          Sequence 2, Application US/09120601
Patent No. 6207413
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: MOUSE
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US-09-071-224-17
                                                                                                         US-09-120-601-2
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTPGAHGETFLHTNYSLKYKLRWYGQDNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEAT 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GSGAHTAVISPODPILLIGSSLLATCSVHGDPPGATAEGLYWTLXGRRLPPELSRVLNAS
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 MOKSHKTRNODEGILPSGRRGTARGPAR 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 MOKSHKTRNODEGILPSGRRGTARGPAR 421
                                                                                                                                                   CLALING LALLON:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTATION NUMBER: 32,743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 FGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 EKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 HIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSV 254
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                                                                                                                                                                                                                                                                                                                                                                                                                 18 PLLPL---LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPPGATAEGLY
                                                                                                                                                                                                                                                                                                                                                                             Gaps
APPLICANT: Oppmann, Birgit
APPLICANT: Timans, Jacqueline C.
APPLICANT: Kastel of Roadeline C.
APPLICANT: Kastel of Roadeline C.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
FILE REFERENCE: DESTANDED OF THE REFERENCE: DESTANDED OF THE REFERENCE: DESTANDED OF THE REFERENCE DESTANDED OF THE REFERENCE DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                       Length 407;
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; Sequence 4, Application US/09012072
; Patent No. 6060276
; GENERAL INFORMATION:
; APPLICANT: Maaiakowski, Piotr
TILLE OF INVENTION: No. 6060276e1 Orphan Receptors
; FILE REPERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/012,072
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                Score 2095; DB 2;
Pred. No. 6.4e-193;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                    91.5%;
95.1%;
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Best Local Similarity 94.4
Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                Query Match 91.5
Best Local Similarity 95.1
Matches 386; Conservative
                                                                                                                                                                                                                                                                         ORGANISM: rodent
US-09-521-335-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: HUMAN
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US-09-012-072-4
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15 RPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGL

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240
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                                                                                                                                                                               VIIDEPEDVHVSRVGGLEDOLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSN 300
                       133
                                              120
                                                                    PEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 193
                                                                                                                   .--V 231
1 RPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGL 60
                                                                                                                                 YWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLP
                                    61 YWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLP
                                                                                                                                                                 VITDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSN
                                                                                                                                                                                                                                                           CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILD.
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: 16560 STIC-Biotech/ChemLib

184613

From:

Woodward, Michael

Sent:

Friday, April 07, 2006 1:46 PM

To:

STIC-Biotech/ChemLib

Cc:

Hamud, Fozia

Subject:

FW: rush search 09/037, 657

Please put in mush queue.

-----Original Message-----

From:

Hamud, Fozia

Sent: To:

Friday, April 07, 2006 1:38 PM

Cc:

Woodward, Michael Chan, Christina

Subject:

rush search 09/037, 657

Hi Mr.Woodward,

Would you kindly approve this rush search? It is a very old case in my docket. The claims are allowable. However, Applicant is running out of time by Thursday the 13th of April. An interference search must be done before then. thanks.

Kindly search SEQ ID NOs: 13, 15 and 44 of 09/037,657 against commercial and interference data bases. Thank you very much.

FOZIA HAMUD PATENT EXAMINER ART UNIT 1647 ROOM:REM 4D64 MAIL BOX: REM 4C70

Searcher: Searcher Phone: Date Searcher Picked up: Date completed:_ Searcher Prep Time:_ Online Time:_

Type of Search AA#: Oligomer: Encode/Transl: Structure #:_ Text: Inventor:___ Litigation: Vendors and cost where applicable STN: DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS: SEQUENCE SYSTEM: WWW/Internet:_ Other (Specify):_

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